

C 539	16	0.3	1299	3	US-09-385-028-21	Sequence 21, Appl	612	16	0.3	1577	4	US-08-979-847B-83	Sequence 83, Appl
C 540	16	0.3	1299	4	US-09-387-413-A	Sequence 21, Appl	C 613	16	0.3	1600	3	US-09-032-372-7	Sequence 7, Appl
C 541	16	0.3	1299	4	US-09-726-614-21	Sequence 21, Appl	C 614	16	0.3	1617	4	US-09-444-336-4	Sequence 4, Appl
C 542	16	0.3	1299	4	US-09-385-040-21	Sequence 21, Appl	C 615	16	0.3	1630	4	US-09-252-991A-10368	Sequence 10368, A
C 543	16	0.3	1299	4	US-09-385-040-21	Sequence 21, Appl	C 616	16	0.3	1639	4	US-09-252-991A-11733	Sequence 11733, A
C 544	16	0.3	1299	4	US-09-500-565-5	Sequence 5, Appl	C 617	16	0.3	1632	4	US-09-252-991A-14532	Sequence 14532, A
C 545	16	0.3	1299	4	US-09-910-823B-5	Sequence 5, Appl	C 618	16	0.3	1647	4	US-09-252-991A-12387	Sequence 12387, A
C 546	16	0.3	1299	4	US-09-910-823B-5	Sequence 5, Appl	C 619	16	0.3	1650	4	US-09-489-039A-1643	Sequence 1643, Ap
C 547	16	0.3	1299	4	US-09-489-039A-3231	Sequence 3231, Ap	C 620	16	0.3	1652	2	US-08-663-566A-12	Sequence 12, Appl
C 548	16	0.3	1299	4	US-09-395-674B-1	Sequence 1, Appl	C 621	16	0.3	1652	2	US-08-023-610-12	Sequence 12, Appl
C 549	16	0.3	1299	4	US-09-489-039A-3422	Sequence 3422, Ap	C 622	16	0.3	1652	2	US-08-362-240A-12	Sequence 12, Appl
C 550	16	0.3	1299	4	US-09-194-942A-12	Sequence 12, Appl	C 623	16	0.3	1652	2	US-08-804-372A-10	Sequence 10, Appl
C 551	16	0.3	1299	4	US-08-415-655-14	Sequence 14, Appl	C 624	16	0.3	1652	3	PCT-US93-10245-12	Sequence 12, Appl
C 552	16	0.3	1299	4	US-07-618-312A-3	Sequence 3, Appl	C 625	16	0.3	1656	4	US-09-304-615-13	Sequence 13, Appl
C 553	16	0.3	1299	4	US-08-280-228-3	Sequence 3, Appl	C 626	16	0.3	1656	4	US-09-870-956-3	Sequence 3, Appl
C 554	16	0.3	1299	4	US-09-252-991A-12209	Sequence 12209, A	C 627	16	0.3	1656	4	US-09-023-655-815	Sequence 815, App
C 555	16	0.3	1299	4	US-09-489-039A-1180	Sequence 1180, Ap	C 628	16	0.3	1658	4	US-09-252-991A-11226	Sequence 11226, A
C 556	16	0.3	1299	4	US-09-420-312D-21	Sequence 21, Appl	C 629	16	0.3	1658	4	US-09-599-287A-1	Sequence 1, Appl
C 557	16	0.3	1299	4	US-09-142-469-1	Sequence 1, Appl	C 630	16	0.3	1658	4	US-09-599-287A-1	Sequence 1, Appl
C 558	16	0.3	1299	4	US-09-252-991A-12249	Sequence 12249, A	C 631	16	0.3	1701	3	US-08-599-268-2	Sequence 2, Appl
C 559	16	0.3	1299	4	US-08-957-302A-3	Sequence 3, Appl	C 632	16	0.3	1704	4	US-09-489-039A-3097	Sequence 3097, Ap
C 560	16	0.3	1299	4	US-09-542-403-3	Sequence 3, Appl	C 633	16	0.3	1705	4	US-09-227-595-23	Sequence 23, Appl
C 561	16	0.3	1299	4	US-08-604-989A-9	Sequence 9, Appl	C 634	16	0.3	1707	4	US-09-489-039A-6584	Sequence 6584, A
C 562	16	0.3	1299	4	US-09-252-991A-15152	Sequence 15152, A	C 635	16	0.3	1711	4	US-09-976-594-497	Sequence 497, App
C 563	16	0.3	1299	4	US-09-252-991A-12361	Sequence 12361, A	C 636	16	0.3	1713	2	US-08-467-947A-1	Sequence 1, Appl
C 564	16	0.3	1299	4	US-09-252-991A-12361	Sequence 12361, A	C 637	16	0.3	1713	4	US-08-467-947A-1	Sequence 1, Appl
C 565	16	0.3	1299	4	US-09-252-991A-4995	Sequence 4995, App	C 638	16	0.3	1713	4	US-09-741-154-1	Sequence 1, Appl
C 566	16	0.3	1299	4	US-09-252-991A-4995	Sequence 4995, App	C 639	16	0.3	1714	4	US-09-620-912D-995	Sequence 995, Appl
C 567	16	0.3	1299	4	PCT-US93-11404-1	Sequence 1, Appl	C 640	16	0.3	1714	4	US-09-620-912D-995	Sequence 1, Appl
C 568	16	0.3	1299	4	US-09-252-991A-8578	Sequence 8578, Ap	C 641	16	0.3	1755	2	US-08-317-785-1	Sequence 1, Appl
C 569	16	0.3	1299	4	US-09-252-991A-14615	Sequence 14615, A	C 642	16	0.3	1755	2	US-09-148-545-112	Sequence 112, Appl
C 570	16	0.3	1299	4	US-08-247-908A-1	Sequence 1, Appl	C 643	16	0.3	1755	4	US-09-049-672A-22	Sequence 22, Appl
C 571	16	0.3	1299	4	US-08-247-908A-1	Sequence 1, Appl	C 644	16	0.3	1831	3	US-09-422-576A-1	Sequence 1, Appl
C 572	16	0.3	1299	4	US-08-326-885A-1	Sequence 1, Appl	C 645	16	0.3	1831	4	US-09-252-991A-1136	Sequence 1136, A
C 573	16	0.3	1299	4	PCT-US94-05290-1	Sequence 1, Appl	C 646	16	0.3	1833	4	US-09-252-991A-1136	Sequence 1136, A
C 574	16	0.3	1299	4	US-09-489-039A-3623	Sequence 3623, Ap	C 647	16	0.3	1842	4	US-09-801-052-1	Sequence 1, Appl
C 575	16	0.3	1299	4	US-09-252-991A-14833	Sequence 14833, A	C 648	16	0.3	1872	4	US-09-801-052-1	Sequence 1, Appl
C 576	16	0.3	1299	4	US-09-252-991A-8971	Sequence 8971, A	C 649	16	0.3	1872	4	US-10-020-121-1	Sequence 121, Ap
C 577	16	0.3	1299	4	US-09-252-991A-11508	Sequence 11508, A	C 650	16	0.3	1886	4	US-09-149-476-93	Sequence 93, Appl
C 578	16	0.3	1299	4	US-09-328-352-270	Sequence 270, App	C 651	16	0.3	1887	4	US-09-252-991A-15156	Sequence 15156, A
C 579	16	0.3	1299	4	US-09-023-655-81	Sequence 81, Appl	C 652	16	0.3	1910	3	US-08-676-882-1	Sequence 1, Appl
C 580	16	0.3	1299	4	US-09-489-039A-5109	Sequence 5109, Ap	C 653	16	0.3	1910	3	US-08-676-882-1	Sequence 1, Appl
C 581	16	0.3	1299	4	US-09-328-352-3051	Sequence 3051, Ap	C 654	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 582	16	0.3	1299	4	US-09-252-991A-14879	Sequence 14879, A	C 655	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 583	16	0.3	1299	4	US-09-252-991A-15378	Sequence 15378, A	C 656	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 584	16	0.3	1299	4	US-09-252-991A-9117	Sequence 9117, Ap	C 657	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 585	16	0.3	1299	4	US-08-601-435-1	Sequence 1, Appl	C 658	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 586	16	0.3	1299	4	US-08-931-047-1	Sequence 1, Appl	C 659	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 587	16	0.3	1299	4	US-08-783-202-1	Sequence 1, Appl	C 660	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 588	16	0.3	1299	4	US-08-878-989-10	Sequence 10, Appl	C 661	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 589	16	0.3	1299	4	US-09-272-796-10	Sequence 10, Appl	C 662	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 590	16	0.3	1299	4	US-09-272-796-10	Sequence 10, Appl	C 663	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 591	16	0.3	1299	4	US-09-134-001C-1333	Sequence 1333, Ap	C 664	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 592	16	0.3	1299	4	US-07-973-324A-7	Sequence 7, Appl	C 665	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 593	16	0.3	1299	4	US-08-343-380-7	Sequence 7, Appl	C 666	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 594	16	0.3	1299	4	US-09-072-435-7	Sequence 7, Appl	C 667	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 595	16	0.3	1299	4	US-09-072-435-7	Sequence 7, Appl	C 668	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 596	16	0.3	1299	4	US-08-604-989A-10	Sequence 10, Appl	C 669	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 597	16	0.3	1299	4	US-09-620-312D-296	Sequence 296, App	C 670	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 598	16	0.3	1299	4	US-09-131-831B-2	Sequence 2, Appl	C 671	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 599	16	0.3	1299	4	US-09-444-336-3	Sequence 3, Appl	C 672	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 600	16	0.3	1299	4	US-09-058-725B-6	Sequence 6, Appl	C 673	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 601	16	0.3	1299	4	US-09-232-657-6	Sequence 6, Appl	C 674	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 602	16	0.3	1299	4	US-08-809-999D-1	Sequence 1, Appl	C 675	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 603	16	0.3	1299	4	US-09-069-637-1	Sequence 1, Appl	C 676	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 604	16	0.3	1299	4	US-09-322-360-1	Sequence 1, Appl	C 677	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 605	16	0.3	1299	4	US-09-131-831B-1	Sequence 1, Appl	C 678	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 606	16	0.3	1299	4	US-08-116-231B-1	Sequence 1, Appl	C 679	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 607	16	0.3	1299	4	US-09-057-435-7	Sequence 7, Appl	C 680	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 608	16	0.3	1299	4	US-09-072-435-7	Sequence 7, Appl	C 681	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 609	16	0.3	1299	4	US-08-604-989A-10	Sequence 10, Appl	C 682	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 610	16	0.3	1299	4	US-09-620-312D-296	Sequence 296, App	C 683	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl
C 611	16	0.3	1299	4	US-09-131-831B-2	Sequence 2, Appl	C 684	16	0.3	1910	3	US-09-315-828-1	Sequence 1, Appl

C 685	16	0.3	2104	4	US-09-023-655-1191	Sequence 1191, Ap	C 758	16	0.3	2646	4	US-09-184-418C-86	Sequence 86, Appl
C 686	16	0.3	2131	4	US-09-420-132-145	Sequence 145, App	C 759	16	0.3	2655	4	US-09-016-433-1094	Sequence 1094, Appl
C 687	16	0.3	2132	2	US-09-159-385-3	Sequence 3, Appl	C 760	16	0.3	2655	4	US-09-023-655-916	Sequence 916, Appl
C 688	16	0.3	2133	4	US-09-186-877-3	Sequence 3, Appl	C 761	16	0.3	2657	4	US-09-488-671-3	Sequence 3, Appl
C 689	16	0.3	2135	4	US-09-221-0178-1091	Sequence 1091, Ap	C 762	16	0.3	2664	2	US-08-942-81-1	Sequence 1, Appl
C 690	16	0.3	2136	4	US-09-023-655-1144	Sequence 1144, Ap	C 763	16	0.3	2664	4	US-09-522-955A-1	Sequence 1, Appl
C 691	16	0.3	2148	4	US-08-809-999-2	Sequence 2, Appl	C 764	16	0.3	2675	1	US-08-070-165F-5	Sequence 5, Appl
C 692	16	0.3	2148	3	US-09-069-637-2	Sequence 2, Appl	C 765	16	0.3	2675	2	US-08-885-418-5	Sequence 5, Appl
C 693	16	0.3	2148	3	US-09-322-360-2	Sequence 2, Appl	C 766	16	0.3	2681	1	US-08-070-165F-9	Sequence 9, Appl
C 694	16	0.3	2153	3	US-08-286-870A-7	Sequence 7, Appl	C 767	16	0.3	2681	2	US-08-885-418-9	Sequence 9, Appl
C 695	16	0.3	2156	4	US-09-452-991A-11722	Sequence 11722, A	C 768	16	0.3	2687	4	US-09-489-847-57	Sequence 57, Appl
C 696	16	0.3	2181	4	US-09-489-847-97	Sequence 97, Appl	C 769	16	0.3	2688	4	US-09-489-039A-722	Sequence 722, Appl
C 697	16	0.3	2208	5	PCT-US95-08493-1	Sequence 1, Appl	C 770	16	0.3	2691	4	US-09-489-039A-3091	Sequence 3091, Ap
C 698	16	0.3	2212	3	US-08-960-507-18	Sequence 18, Appl	C 771	16	0.3	2692	3	US-08-981-39-11	Sequence 11, App
C 699	16	0.3	2212	4	US-09-136-801-18	Sequence 18, Appl	C 772	16	0.3	2697	4	US-09-212-247C-10	Sequence 10, Appl
C 700	16	0.3	2212	4	US-09-302-088A-18	Sequence 18, Appl	C 773	16	0.3	2712	4	US-09-919-117-40	Sequence 40, Appl
C 701	16	0.3	2240	4	US-09-489-847-84	Sequence 84, Appl	C 774	16	0.3	2718	3	US-09-474-658-69	Sequence 69, App
C 702	16	0.3	2254	3	US-08-552-369-1	Sequence 1, Appl	C 775	16	0.3	2736	4	US-09-252-991A-8666	Sequence 8666, App
C 703	16	0.3	2280	3	US-09-009-913-8	Sequence 8, Appl	C 776	16	0.3	2763	4	US-09-252-991A-12347	Sequence 12347, A
C 704	16	0.3	2283	4	US-09-352-991A-10956	Sequence 10956, A	C 777	16	0.3	2823	4	US-09-704-611-4	Sequence 4, Appl
C 705	16	0.3	2292	4	US-09-328-352-280	Sequence 280, App	C 778	16	0.3	2834	4	US-09-566-921-43	Sequence 43, Appl
C 706	16	0.3	2299	4	US-09-475-515-81	Sequence 81, Appl	C 779	16	0.3	2857	3	US-08-981-39-14	Sequence 4, Appl
C 707	16	0.3	2300	4	US-09-475-515-81	Sequence 81, Appl	C 780	16	0.3	2865	2	US-08-749-169A-2	Sequence 2, Appl
C 708	16	0.3	2305	4	US-08-979-847B-87	Sequence 87, Appl	C 781	16	0.3	2865	2	US-09-130-033A-2	Sequence 2, Appl
C 709	16	0.3	2305	4	US-09-475-515-80	Sequence 80, Appl	C 782	16	0.3	2869	1	US-08-374-83-3	Sequence 2, Appl
C 710	16	0.3	2306	4	US-09-475-515-82	Sequence 82, Appl	C 783	16	0.3	2869	1	US-08-644-271-2	Sequence 2, Appl
C 711	16	0.3	2311	4	US-09-489-847-123	Sequence 123, Appl	C 784	16	0.3	2869	4	US-09-077-995-2	Sequence 2, Appl
C 712	16	0.3	2312	4	US-09-475-515-84	Sequence 84, Appl	C 785	16	0.3	2881	4	US-09-702-703-1194	Sequence 1794, Ap
C 713	16	0.3	2313	4	US-09-970-838-157	Sequence 157, App	C 786	16	0.3	2881	4	US-09-736-457-1794	Sequence 1794, Ap
C 714	16	0.3	2320	4	US-09-976-594-428	Sequence 428, App	C 787	16	0.3	2881	4	US-09-671-322-1794	Sequence 1794, Ap
C 715	16	0.3	2367	4	US-09-352-991A-726	Sequence 726, App	C 788	16	0.3	2892	4	US-09-704-611-3	Sequence 3, Appl
C 716	16	0.3	2370	4	US-09-252-991A-13196	Sequence 12196, A	C 789	16	0.3	2899	4	US-08-981-39-129-24	Sequence 24, Appl
C 717	16	0.3	2379	4	US-09-352-991A-686	Sequence 686, App	C 790	16	0.3	2914	1	US-08-454-097-11	Sequence 11, Appl
C 718	16	0.3	2394	4	US-09-620-312D-592	Sequence 592, App	C 791	16	0.3	2914	3	US-08-185-35-11	Sequence 11, Appl
C 719	16	0.3	2433	4	US-09-016-434-1469	Sequence 1469, Ap	C 792	16	0.3	2925	4	US-09-883-133-6	Sequence 6, Appl
C 720	16	0.3	2436	4	US-09-620-312D-566	Sequence 566, App	C 793	16	0.3	2943	4	US-09-022-011B-153	Sequence 153, App
C 721	16	0.3	2446	3	US-09-009-913-6	Sequence 6, Appl	C 794	16	0.3	2991	4	US-09-252-991A-12025	Sequence 12025, A
C 722	16	0.3	2430	4	US-09-620-312D-591	Sequence 591, App	C 795	16	0.3	2997	2	US-08-453-86-1	Sequence 1, Appl
C 723	16	0.3	2441	4	US-09-785-381-4	Sequence 4, Appl	C 796	16	0.3	2997	2	US-08-452-734A-1	Sequence 1, Appl
C 724	16	0.3	2454	3	US-08-890-615-1	Sequence 1, Appl	C 797	16	0.3	2997	3	US-08-176-401B-1	Sequence 1, Appl
C 725	16	0.3	2454	4	US-09-346-290A-1	Sequence 1, Appl	C 798	16	0.3	2997	5	PCT-US94-14989-1	Sequence 1, Appl
C 726	16	0.3	2457	4	US-09-872-733A-3	Sequence 3, Appl	C 799	16	0.3	3012	4	US-09-252-991A-7498	Sequence 7498, Ap
C 727	16	0.3	2459	4	US-09-352-991A-12963	Sequence 12963, A	C 800	16	0.3	3017	1	US-08-444-739-1	Sequence 1, Appl
C 728	16	0.3	2475	3	US-09-043-185-1	Sequence 1, Appl	C 801	16	0.3	3017	1	US-08-445-04-1	Sequence 1, Appl
C 729	16	0.3	2475	3	US-09-045-185-3	Sequence 3, Appl	C 802	16	0.3	3032	4	US-09-193-562D-33	Sequence 33, App
C 730	16	0.3	2475	4	US-09-579-365-1	Sequence 1, Appl	C 803	16	0.3	3032	4	US-09-021-011B-347	Sequence 347, App
C 731	16	0.3	2482	1	US-07-803-622B-1	Sequence 1, Appl	C 804	16	0.3	3037	2	US-08-938-365-1	Sequence 1, Appl
C 732	16	0.3	2483	4	US-09-352-991A-11987	Sequence 11987, A	C 805	16	0.3	3057	3	US-09-150-460B-5	Sequence 5, Appl
C 733	16	0.3	2489	4	US-09-009-913-10	Sequence 10, Appl	C 806	16	0.3	3059	4	US-09-770-959A-2	Sequence 2, Appl
C 734	16	0.3	2499	3	US-09-352-991A-696	Sequence 696, App	C 807	16	0.3	3120	4	US-09-252-991A-12395	Sequence 12395, A
C 735	16	0.3	2508	4	US-09-758-282B-48	Sequence 48, Appl	C 808	16	0.3	3141	4	US-09-489-039A-977	Sequence 977, App
C 736	16	0.3	2508	4	US-09-758-282B-242	Sequence 242, App	C 809	16	0.3	3147	2	US-08-781-802-7	Sequence 7, Appl
C 737	16	0.3	2510	2	US-08-888-982A-42	Sequence 42, Appl	C 810	16	0.3	3147	3	US-08-694-078-7	Sequence 7, Appl
C 738	16	0.3	2510	4	US-09-462-661-42	Sequence 42, Appl	C 811	16	0.3	3147	3	US-08-694-078-7	Sequence 7, Appl
C 739	16	0.3	2510	4	US-09-506-073-89	Sequence 89, Appl	C 812	16	0.3	3147	6	5196511-1	Patent No. 5196511-1
C 740	16	0.3	2519	1	US-08-470-720-2	Sequence 2, Appl	C 813	16	0.3	3175	4	US-09-023-655-1185	Sequence 1185, Ap
C 741	16	0.3	2577	2	US-08-309-521-25	Sequence 25, Appl	C 814	16	0.3	3336	4	US-09-833-381-1727	Sequence 1727, Appl
C 742	16	0.3	2577	4	US-09-365-503B-135	Sequence 135, App	C 815	16	0.3	3390	4	US-09-851-896-10	Sequence 10, Appl
C 743	16	0.3	2580	5	PCT-US95-08493-18	Sequence 18, App	C 816	16	0.3	3391	1	US-08-574-763-1	Sequence 1, Appl
C 744	16	0.3	2582	4	US-09-489-039A-3008	Sequence 3008, Ap	C 817	16	0.3	3393	4	US-09-409-648-5	Sequence 5, Appl
C 745	16	0.3	2595	4	US-09-023-655-254	Sequence 254, App	C 818	16	0.3	3393	4	US-09-409-648-6	Sequence 6, Appl
C 746	16	0.3	2604	4	US-09-540-336-756	Sequence 756, App	C 819	16	0.3	3319	2	US-08-960-022-19	Sequence 19, Appl
C 747	16	0.3	2604	5	PCT-US95-08493-20	Sequence 20, Appl	C 820	16	0.3	3324	4	US-09-620-312D-1020	Sequence 1020, Appl
C 748	16	0.3	2610	1	US-08-374-83A-17	Sequence 17, Appl	C 821	16	0.3	3324	4	US-09-489-039A-719	Sequence 719, Ap
C 749	16	0.3	2610	1	US-08-644-271-28	Sequence 28, Appl	C 822	16	0.3	3396	3	US-08-974-549A-640	Sequence 640, Appl
C 750	16	0.3	2610	4	US-09-077-955-32	Sequence 32, Appl	C 823	16	0.3	3396	3	US-08-974-549A-641	Sequence 641, Appl
C 751	16	0.3	2634	2	US-08-818-514-1	Sequence 1, Appl	C 824	16	0.3	3396	4	US-09-721-456-641	Sequence 641, Appl
C 752	16	0.3	2634	2	US-08-818-514-1	Sequence 1, Appl	C 825	16	0.3	3396	4	US-09-721-456-641	Sequence 641, Appl
C 753	16	0.3	2634	3	US-09-115-934A-1	Sequence 1, Appl	C 826	16	0.3	3417	4	US-09-252-991A-3720	Sequence 3720, Ap
C 754	16	0.3	2634	3	US-09-115-934A-2	Sequence 2, Appl	C 827	16	0.3	3441	4	US-09-866-028-6	Sequence 6, Appl
C 755	16	0.3	2634	4	US-09-611-175-1	Sequence 1, Appl	C 828	16	0.3	3441	4	US-09-866-028-6	Sequence 6, Appl
C 756	16	0.3	2634	4	US-09-611-175-2	Sequence 2, Appl	C 829	16	0.3	3458	4	US-09-023-655-603	Sequence 603, Appl
C 757	16	0.3	2640	4	US-08-884-932A-37	Sequence 37, Appl	C 830	16	0.3	3465	4	US-09-134-001C-591	Sequence 591, Appl

831	16	0.3	3475	3	US-09-657-481A-10	Sequence 10, Appl	C 904	16	0.3	4500	1	US-08-308-872B-1	Sequence 1, Appl
832	16	0.3	3476	3	US-08-630-916A-47	Sequence 47, Appl	905	16	0.3	4650	1	US-07-998-003A-102	Sequence 102, App
833	16	0.3	3483	4	US-09-130-491-3	Sequence 3, Appl	906	16	0.3	4650	1	US-08-453-274B-102	Sequence 102, App
C 834	16	0.3	3577	4	US-09-620-312D-457	Sequence 457, App	907	16	0.3	4650	1	US-08-453-695A-102	Sequence 102, App
835	16	0.3	3600	1	US-08-537-002A-5	Sequence 5, Appl	908	16	0.3	4650	1	US-08-268-161A-102	Sequence 102, App
836	16	0.3	3600	3	US-08-863-010-5	Sequence 5, Appl	909	16	0.3	4650	2	US-08-453-102A-102	Sequence 102, App
837	16	0.3	3600	3	US-09-024-429-5	Sequence 5, Appl	910	16	0.3	4650	3	US-09-089-639-102	Sequence 102, App
838	16	0.3	3621	4	US-09-635-872A-21	Sequence 21, Appl	911	16	0.3	4650	5	PCT-US93-12588-102	Sequence 102, App
839	16	0.3	3621	4	US-09-636-077A-21	Sequence 21, Appl	912	16	0.3	4650	5	PCT-US93-08071-102	Sequence 102, App
840	16	0.3	3621	4	US-09-636-060C-21	Sequence 21, Appl	913	16	0.3	4656	3	US-09-150-460B-4	Sequence 4, Appl
841	16	0.3	3623	4	US-09-986-552-23	Sequence 23, Appl	914	16	0.3	4900	1	US-08-245-295-5	Sequence 5, Appl
842	16	0.3	3623	1	US-08-306-691B-35	Sequence 35, Appl	C 915	16	0.3	4900	1	US-08-481-130-5	Sequence 5, Appl
C 843	16	0.3	3636	3	US-09-074-579-2	Sequence 2, Appl	C 916	16	0.3	4900	1	US-08-656-984-5	Sequence 5, Appl
C 844	16	0.3	3636	3	US-09-388-774-2	Sequence 2, Appl	C 917	16	0.3	4900	1	US-08-485-604-5	Sequence 5, Appl
C 845	16	0.3	3657	4	US-09-252-991A-8298	Sequence 8298, App	C 918	16	0.3	4900	2	US-08-487-595-5	Sequence 26, Appl
C 846	16	0.3	3660	4	US-09-252-991A-12269	Sequence 12269, A	C 919	16	0.3	4900	3	US-08-683-790-26	Sequence 26, Appl
C 847	16	0.3	3710	3	US-07-741-453A-62	Sequence 62, Appl	C 920	16	0.3	4900	3	US-08-631-097-3	Sequence 3, Appl
C 848	16	0.3	3747	4	US-09-213-293D-2	Sequence 2, Appl	C 921	16	0.3	4935	2	US-08-470-720-5	Sequence 5, Appl
C 849	16	0.3	3754	4	US-08-586-740A-6	Sequence 6, Appl	C 922	16	0.3	4964	1	US-08-470-720-5	Sequence 5, Appl
C 850	16	0.3	3754	4	US-08-579-611-17	Sequence 17, Appl	C 923	16	0.3	5049	1	US-08-336-345-1	Sequence 2, Appl
C 851	16	0.3	3769	4	US-08-379-611-18	Sequence 18, Appl	924	16	0.3	5049	1	US-08-336-345-2	Sequence 2, Appl
852	16	0.3	3770	4	US-09-566-921-53	Sequence 53, Appl	925	16	0.3	5049	2	US-08-647-655-1	Sequence 2, Appl
853	16	0.3	3783	4	US-09-635-872A-20	Sequence 20, Appl	C 926	16	0.3	5049	2	US-08-647-655-2	Sequence 2, Appl
854	16	0.3	3783	4	US-09-636-077A-20	Sequence 20, Appl	C 927	16	0.3	5077	1	US-08-245-295-8	Sequence 8, Appl
855	16	0.3	3783	4	US-09-636-060C-20	Sequence 20, Appl	C 928	16	0.3	5077	1	US-08-481-130-8	Sequence 8, Appl
856	16	0.3	3783	4	US-09-986-552-20	Sequence 20, Appl	C 929	16	0.3	5077	1	US-08-485-984-8	Sequence 8, Appl
857	16	0.3	3805	4	US-09-220-132-9	Sequence 9, Appl	C 930	16	0.3	5077	1	US-08-485-604-8	Sequence 8, Appl
858	16	0.3	3821	4	US-09-566-921-25	Sequence 25, Appl	C 931	16	0.3	5077	2	US-08-487-595-8	Sequence 8, Appl
C 859	16	0.3	3825	6	5310678-2	Patent No. 5310678	C 932	16	0.3	5091	4	US-08-469-260A-668	Sequence 668, App
860	16	0.3	3839	4	US-09-898-361-10	Sequence 10, Appl	C 933	16	0.3	5091	4	US-08-488-446-668	Sequence 668, App
861	16	0.3	3861	4	US-09-252-991A-8018	Sequence 8018, App	C 934	16	0.3	5247	1	US-08-467-344A-668	Sequence 668, App
862	16	0.3	3886	4	US-09-328-352-1919	Sequence 1919, App	C 935	16	0.3	5247	1	US-08-920-812-15	Sequence 15, Appl
C 863	16	0.3	3925	2	US-09-047-026A-3	Sequence 3, Appl	C 936	16	0.3	5247	1	US-08-920-812-15	Sequence 15, Appl
C 864	16	0.3	3936	4	US-09-919-172-49	Sequence 49, Appl	C 937	16	0.3	5247	1	US-08-921-177-15	Sequence 15, Appl
865	16	0.3	4031	1	US-08-159-784-1	Sequence 1, Appl	C 938	16	0.3	5247	1	US-08-362-577C-15	Sequence 15, Appl
C 866	16	0.3	4079	4	US-09-016-434-113	Sequence 113, App	C 939	16	0.3	5247	2	US-08-920-812-15	Sequence 15, Appl
867	16	0.3	4104	1	US-07-998-003A-94	Sequence 94, Appl	C 940	16	0.3	5275	1	US-08-485-588-1	Sequence 1, Appl
868	16	0.3	4104	1	US-08-453-274B-94	Sequence 94, Appl	C 941	16	0.3	5275	1	US-08-484-565-1	Sequence 1, Appl
869	16	0.3	4104	1	US-08-453-695A-94	Sequence 94, Appl	C 942	16	0.3	5275	2	US-08-480-751-1	Sequence 1, Appl
870	16	0.3	4104	2	US-08-268-161A-94	Sequence 94, Appl	C 943	16	0.3	5275	2	US-08-943-866-1	Sequence 1, Appl
871	16	0.3	4104	2	US-08-453-702A-94	Sequence 94, Appl	C 944	16	0.3	5275	3	US-08-353-784-1	Sequence 1, Appl
872	16	0.3	4104	3	US-09-099-639-94	Sequence 94, Appl	C 945	16	0.3	5275	3	US-08-464-179B-1	Sequence 1, Appl
873	16	0.3	4104	5	PCT-US93-12588-94	Sequence 94, Appl	C 946	16	0.3	5275	4	US-08-484-159-1	Sequence 1, Appl
874	16	0.3	4104	5	PCT-US95-08071-94	Sequence 94, Appl	C 947	16	0.3	5357	4	US-09-392-184-5	Sequence 5, Appl
875	16	0.3	4113	4	US-09-785-381-2	Sequence 2, Appl	C 948	16	0.3	5357	6	5223424-5	Patent No. 5223424
C 876	16	0.3	4143	4	US-09-328-352-4006	Sequence 4006, App	C 949	16	0.3	5400	4	US-09-134-000C-1773	Sequence 1773, App
C 877	16	0.3	4177	2	US-08-484-575A-12	Sequence 12, Appl	950	16	0.3	5400	4	US-09-635-872A-4	Sequence 4, Appl
C 878	16	0.3	4177	3	US-08-477-459-12	Sequence 12, Appl	951	16	0.3	5497	4	US-09-636-077A-4	Sequence 4, Appl
C 879	16	0.3	4177	3	US-08-479-869-12	Sequence 12, Appl	952	16	0.3	5497	4	US-09-636-060C-4	Sequence 4, Appl
C 880	16	0.3	4177	3	US-08-486-414-12	Sequence 12, Appl	953	16	0.3	5597	4	US-09-986-552-4	Sequence 4, Appl
C 881	16	0.3	4177	5	PCT-US94-01826A-12	Sequence 12, Appl	954	16	0.3	5605	2	US-09-268-140-6	Sequence 2, Appl
C 882	16	0.3	4177	5	PCT-US94-02252A-12	Sequence 12, Appl	955	16	0.3	5690	3	US-08-447-464-2	Sequence 2, Appl
C 883	16	0.3	4190	3	US-08-589-291A-2	Sequence 2, Appl	956	16	0.3	5690	2	US-08-716-679-2	Sequence 2, Appl
884	16	0.3	4190	4	US-09-589-619-2	Sequence 2, Appl	957	16	0.3	5886	3	US-08-810-712-9	Sequence 9, Appl
885	16	0.3	4196	4	US-09-588-188B-19	Sequence 19, Appl	C 958	16	0.3	5962	1	US-08-188-582-10	Sequence 10, Appl
886	16	0.3	4196	4	US-09-291-417D-19	Sequence 19, Appl	C 959	16	0.3	5962	1	US-08-686-715-10	Sequence 10, Appl
887	16	0.3	4319	4	US-09-475-515-6	Sequence 6, Appl	C 960	16	0.3	6049	4	US-08-793-273C-3	Sequence 3, Appl
C 888	16	0.3	4338	4	US-09-872-733A-1	Sequence 1, Appl	961	16	0.3	6049	5	PCT-US95-11684-3	Sequence 3, Appl
C 889	16	0.3	4354	4	US-09-802-927-1	Sequence 1, Appl	C 962	16	0.3	6138	3	US-09-067-800-4	Sequence 4, Appl
C 890	16	0.3	4359	3	US-08-331-625A-1	Sequence 1, Appl	C 963	16	0.3	6138	3	US-09-349-577A-4	Sequence 4, Appl
C 891	16	0.3	4359	4	US-09-494-155A-1	Sequence 1, Appl	964	16	0.3	6136	4	US-09-770-595A-1	Sequence 1, Appl
C 892	16	0.3	4359	4	US-09-572-484-1	Sequence 1, Appl	C 965	16	0.3	6519	1	US-08-588-985-1	Sequence 1, Appl
C 893	16	0.3	4359	5	PCT-US93-04384-17	Sequence 17, Appl	C 966	16	0.3	6519	1	US-09-910-808-1	Sequence 1, Appl
C 894	16	0.3	4359	5	PCT-US93-04692-11	Sequence 11, Appl	967	16	0.3	6614	4	US-09-150-460B-3	Sequence 3, Appl
C 895	16	0.3	4366	4	US-08-586-740A-12	Sequence 12, Appl	968	16	0.3	6644	4	US-08-875-435B-5	Sequence 5, Appl
C 896	16	0.3	4378	4	US-08-586-740A-9	Sequence 9, Appl	969	16	0.3	6814	4	US-09-484-970B-66	Sequence 66, Appl
C 897	16	0.3	4417	3	US-07-741-453A-57	Sequence 57, Appl	C 970	16	0.3	6816	4	US-09-404-650-1	Sequence 1, Appl
C 898	16	0.3	4425	2	US-08-749-169A-1	Sequence 1, Appl	C 971	16	0.3	6816	4	US-09-935-541-1	Sequence 1, Appl
C 899	16	0.3	4425	2	US-09-130-032A-1	Sequence 1, Appl	C 972	16	0.3	6855	4	US-09-404-650-3	Sequence 3, Appl
C 900	16	0.3	4426	1	US-09-658-687A-3	Sequence 3, Appl	C 973	16	0.3	6855	4	US-09-404-650-3	Sequence 3, Appl
C 901	16	0.3	4429	1	US-08-308-872B-3	Sequence 3, Appl	974	16	0.3	6960	2	US-09-935-541-3	Sequence 3, Appl
C 902	16	0.3	4435	1	US-08-308-872B-5	Sequence 5, Appl	975	16	0.3	6960	2	US-08-841-349-3	Sequence 3, Appl
903	16	0.3	4497	4	US-09-252-991A-14663	Sequence 14663, A	976	16	0.3	6960	4	US-09-620-312D-155	Sequence 155, App

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977 16 0.3 7620 1 US-07-767-135-1 Sequence 1, Appli
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979 16 0.3 7898 4 US-08-984-703A-49 Sequence 49, Appli
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981 16 0.3 8176 4 US-09-431-184A-5 Sequence 5, Appli
982 16 0.3 8312 4 US-09-620-312D-1048 Sequence 1048, Ap
983 16 0.3 8366 4 US-09-872-733A-6 Sequence 6, Appli
984 16 0.3 8438 1 US-07-945-283-1 Sequence 1, Appli
985 16 0.3 8598 4 US-08-305-790B-1 Sequence 11, Appli
986 16 0.3 8912 4 US-08-469-260A-11 Sequence 11, Appli
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988 16 0.3 8912 4 US-08-467-344A-11 Sequence 11, Appli
989 16 0.3 8972 4 US-09-184-418C-9 Sequence 9, Appli
990 16 0.3 9034 4 US-08-469-260A-397 Sequence 397, App
991 16 0.3 9034 4 US-08-468-446-397 Sequence 397, App
992 16 0.3 9034 4 US-08-467-344A-397 Sequence 397, App
993 16 0.3 9122 2 US-08-417-629B-1 Sequence 1, Appli
994 16 0.3 9126 1 US-08-580-038-26 Sequence 26, Appli
995 16 0.3 9126 2 US-08-639-857-3 Sequence 3, Appli
996 16 0.3 9143 2 US-08-639-857-32 Sequence 32, Appli
997 16 0.3 9143 4 US-08-469-260A-390 Sequence 390, App
998 16 0.3 9143 4 US-08-469-260A-393 Sequence 393, App
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## ALIGNMENTS

## RESULT 1

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US-09-252-991A-3017/c
; Sequence 3017, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3017
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3017

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1920 GGAGACCGCATGACCTTCG 1939

Db 108 GGAGACCGCATGACCTTCG 89

## RESULT 2

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US-09-313-294A-7021/c
; Sequence 7021, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalundi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600

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; SOFTWARE: PERL Program
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; LENGTH: 311
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381005H1
; NAME/KEY: unsure
; LOCATION: 87, 254, 276, 286
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7021

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Query Match 0.4%; Score 20; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 115 CAACTCCACCGCTCCAGGA 96

## RESULT 3

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US-09-401-064-165/c
; Sequence 165, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.47102
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-401-064-165

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Query Match 0.4%; Score 20; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4827 CAACTCCACCGCTCCAGGA 4846

Db 116 CAACTCCACCGCTCCAGGA 97

## RESULT 4

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US-09-385-982-238/c
; Sequence 238, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31

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NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 238  
LENGTH: 616  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(616)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-238

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Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4827 CAATCCACCGTCTCCAGGA 4846  
DB 71 CAATCCACCGTCTCCAGGA 52

RESULT 5  
US-09-252-991A-2754  
Sequence 2754, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 2754  
LENGTH: 894  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2754

Query Match 0.4%; Score 20; DB 4; Length 894;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 GGAGACCGGCATGACCTTCG 1939  
DB 687 GGAGACCGGCATGACCTTCG 706

RESULT 6  
US-09-252-991A-2651  
Sequence 2651, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 2651  
LENGTH: 1029  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2651

Query Match 0.4%; Score 20; DB 4; Length 1029;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 GGAGACCGGCATGACCTTCG 1939  
DB 361 GGAGACCGGCATGACCTTCG 380

RESULT 7  
US-09-252-991A-3212/C  
Sequence 3212, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 3212  
LENGTH: 1455  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-3212

Query Match 0.4%; Score 20; DB 4; Length 1455;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 GGAGACCGGCATGACCTTCG 1939  
DB 322 GGAGACCGGCATGACCTTCG 303

RESULT 8  
US-09-976-594-779/C  
Sequence 779, Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:  
APPLICANT: Furness, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 779  
LENGTH: 1456  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. 6673549 1384716.4  
NAME/KEY: unsure  
LOCATION: 1453  
OTHER INFORMATION: a, t, c, g, or other  
US-09-976-594-779

Query Match 0.4%; Score 20; DB 4; Length 1456;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4827 CAATCCACCGTCTCCAGGA 4846

Db 425 CAATCCACCGTCTCCAGCA 406

## RESULT 9

US-08-630-915A-31  
Sequence 31, Application US/08630915A  
Patent No. 6309820  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6309820h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
TITLE OF INVENTION: USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,915A  
FILING DATE: 03-Apr-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1636 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-630-915A-31

Query Match 0.4%; Score 20; DB 4; Length 1636;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4179 GCTGCAGACCAAGCTGAGT 4198  
DB 863 GCTGCAGACCAAGCTGAGT 882

RESULT 10  
US-09-620-312D-702/c  
Sequence 702, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyun  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yungang  
APPLICANT: Wang, Dunru  
APPLICANT: Wang, Zhilwei  
APPLICANT: John Tillinghaast  
APPLICANT: Dymnac, Radoje T.  
TITLE OF INVENTION: Polypeptides  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PC\_Fl\_genes Version 1.0  
SEQ ID NO 702  
LENGTH: 2522  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (179)..(1606)  
US-09-620-312D-702

Query Match 0.4%; Score 20; DB 4; Length 2522;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 CACCATGCTGTAAGCTTCA 1907  
DB 517 CACCATGCTGTAAGCTTCA 498

RESULT 11  
US-09-105-537-30/c  
Sequence 30, Application US/09105537A  
Patent No. 6265202  
GENERAL INFORMATION:  
APPLICANT: Sherman, D.H.  
APPLICANT: Liu, H.  
APPLICANT: Xue, Y.  
APPLICANT: Zhao, L.  
TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
FILE REFERENCE: 600.438US1  
CURRENT APPLICATION NUMBER: US/09/105,537A  
CURRENT FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 30  
LENGTH: 13842  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-105-537-30

Query Match 0.4%; Score 20; DB 3; Length 13842;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACGCTCCAGGAC 4847  
DB 10196 AACTCCACGCTCCAGGAC 10177

RESULT 12  
US-09-105-537-5/c  
Sequence 5, Application US/09105537A  
Patent No. 6265202  
GENERAL INFORMATION:

APPLICANT: Sherman, D.H.  
APPLICANT: Liu, H.  
APPLICANT: Xue, Y.  
APPLICANT: Zhao, L.  
TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
FILE REFERENCE: 600,438US1  
CURRENT APPLICATION NUMBER: US/09/105,537A  
CURRENT FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 36778  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-105-537-5

Query Match 0.4%; Score 20; DB 3; Length 36778;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGCTCTCCAGGAC 4847  
DB 11937 AACTCCACCGCTCTCCAGGAC 11918

RESULT 13  
US-09-320-878-19/c  
Sequence 19, Application US/09320878A  
Patent No. 6117659  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/320,878A  
CURRENT FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
EARLIER FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 60/119,139  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: 60/100,880  
EARLIER FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-19

Query Match 0.4%; Score 20; DB 3; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGCTCTCCAGGAC 4847  
DB 10079 AACTCCACCGCTCTCCAGGAC 10060

RESULT 14  
US-09-141-908-1/c  
Sequence 1, Application US/09141908  
Patent No. 6503741  
GENERAL INFORMATION:

APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a  
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold  
FILE REFERENCE: 300622002100  
CURRENT APPLICATION NUMBER: US/09/141,908  
CURRENT FILING DATE: 1998-06-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: PROV. 60/076,919  
EARLIER FILING DATE: 1998-03-05  
EARLIER APPLICATION NUMBER: PROV. 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-141-908-1

Query Match 0.4%; Score 20; DB 4; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGCTCTCCAGGAC 4847  
DB 10079 AACTCCACCGCTCTCCAGGAC 10060

RESULT 15  
US-09-657-440-19/c  
Sequence 19, Application US/09657440  
Patent No. 6509455  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/657,440  
CURRENT FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: 09/320,878  
PRIOR FILING DATE: 1999-05-27  
PRIOR APPLICATION NUMBER: CIP OF 09/141,908  
PRIOR FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-657-440-19

Query Match 0.4%; Score 20; DB 4; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGCTCTCCAGGAC 4847  
DB 10079 AACTCCACCGCTCTCCAGGAC 10060

Search completed: February 20, 2004, 09:38:27  
Job time : 290 secs

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 07:09:02 ; Search time 1298 Seconds  
(without alignments)  
15352.741 Million cell updates/sec

Title: US-09-964-956-12

Perfect score: 5691  
Sequence: 1 atgaagcagctgcctgaa.....gcttagacgtgaataaa 5691

Scoring table:  
OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2308684 seqs, 1750822206 residues

Word size : 0 4617368

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
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Published Applications NA:\*

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- 2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 10: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 18: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108	19.5	3666	15	US-10-108-260A-802
2	793	13.9	2597	14	US-10-245-103-91
3	793	13.9	2597	14	US-10-245-107-91
4	793	13.9	2597	14	US-10-245-143-91
5	793	13.9	2597	14	US-10-245-171-91
6	793	13.9	2597	14	US-10-245-851-91
7	793	13.9	2597	14	US-10-245-883-91
8	793	13.9	2597	14	US-10-237-535-91
9	793	13.9	2597	14	US-10-238-183-91
10	793	13.9	2597	14	US-10-238-283-91
11	793	13.9	2597	14	US-10-238-370-91
12	793	13.9	2597	14	US-10-245-035-91
13	793	13.9	2597	14	US-10-245-147-91
14	793	13.9	2597	14	US-10-245-730-91
15	793	13.9	2597	14	US-10-245-739-91

16	793	13.9	2597	14	US-10-246-210-91	Sequence 91, Appl
17	793	13.9	2597	14	US-10-239-196-91	Sequence 91, Appl
18	793	13.9	2597	14	US-10-243-024-91	Sequence 91, Appl
19	793	13.9	2597	14	US-10-243-409-91	Sequence 91, Appl
20	793	13.9	2597	14	US-10-245-621-91	Sequence 91, Appl
21	793	13.9	2597	14	US-10-245-880-91	Sequence 91, Appl
22	793	13.9	2597	14	US-10-245-033-91	Sequence 91, Appl
23	793	13.9	2597	14	US-10-243-093-91	Sequence 91, Appl
24	793	13.9	2597	14	US-10-245-185-91	Sequence 91, Appl
25	793	13.9	2597	14	US-10-245-427-91	Sequence 91, Appl
26	793	13.9	2597	14	US-10-245-473-91	Sequence 91, Appl
27	793	13.9	2597	14	US-10-245-770-91	Sequence 91, Appl
28	793	13.9	2597	14	US-10-245-877-91	Sequence 91, Appl
29	793	13.9	2597	14	US-10-246-976-91	Sequence 91, Appl
30	793	13.9	2597	14	US-10-243-320-91	Sequence 91, Appl
31	793	13.9	2597	14	US-10-242-743-91	Sequence 91, Appl
32	793	13.9	2597	14	US-10-242-845-91	Sequence 91, Appl
33	793	13.9	2597	14	US-10-237-636-91	Sequence 91, Appl
34	793	13.9	2597	14	US-10-238-325-91	Sequence 91, Appl
35	793	13.9	2597	14	US-10-238-346-91	Sequence 91, Appl
36	793	13.9	2597	14	US-10-238-411-91	Sequence 91, Appl
37	793	13.9	2597	14	US-10-243-124-91	Sequence 91, Appl
38	793	13.9	2597	14	US-10-243-425-91	Sequence 91, Appl
39	793	13.9	2597	14	US-10-243-446-91	Sequence 91, Appl
40	793	13.9	2597	14	US-10-245-874-91	Sequence 91, Appl
41	793	13.9	2597	14	US-10-242-653-91	Sequence 91, Appl
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43	793	13.9	2597	14	US-10-243-388-91	Sequence 91, Appl
44	793	13.9	2597	14	US-10-244-947-91	Sequence 91, Appl
45	793	13.9	2597	14	US-10-244-968-91	Sequence 91, Appl
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47	793	13.9	2597	14	US-10-245-127-91	Sequence 91, Appl
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56	793	13.9	2597	14	US-10-245-899-91	Sequence 91, Appl
57	793	13.9	2597	14	US-10-247-058-91	Sequence 91, Appl
58	793	13.9	2597	14	US-10-245-454-91	Sequence 91, Appl
59	793	13.9	2597	14	US-10-237-471-91	Sequence 91, Appl
60	793	13.9	2597	14	US-10-238-261-91	Sequence 91, Appl
61	793	13.9	2597	14	US-10-241-860-91	Sequence 91, Appl
62	793	13.9	2597	14	US-10-242-172-91	Sequence 91, Appl
63	793	13.9	2597	14	US-10-242-652-91	Sequence 91, Appl
64	793	13.9	2597	14	US-10-242-990-91	Sequence 91, Appl
65	793	13.9	2597	14	US-10-243-023-91	Sequence 91, Appl
66	793	13.9	2597	14	US-10-243-023-91	Sequence 91, Appl
67	793	13.9	2597	14	US-10-243-023-91	Sequence 91, Appl
68	793	13.9	2597	14	US-10-243-276-91	Sequence 91, Appl
69	793	13.9	2597	14	US-10-243-326-91	Sequence 91, Appl
70	793	13.9	2597	14	US-10-243-364-91	Sequence 91, Appl
71	793	13.9	2597	14	US-10-243-494-91	Sequence 91, Appl
72	793	13.9	2597	14	US-10-244-995-91	Sequence 91, Appl
73	793	13.9	2597	14	US-10-245-230-91	Sequence 91, Appl
74	793	13.9	2597	14	US-10-245-253-91	Sequence 91, Appl
75	793	13.9	2597	14	US-10-245-479-91	Sequence 91, Appl
76	793	13.9	2597	14	US-10-245-499-91	Sequence 91, Appl
77	793	13.9	2597	14	US-10-245-772-91	Sequence 91, Appl
78	793	13.9	2597	14	US-10-245-811-91	Sequence 91, Appl
79	793	13.9	2597	14	US-10-245-812-91	Sequence 91, Appl
80	793	13.9	2597	14	US-10-245-875-91	Sequence 91, Appl
81	793	13.9	2597	14	US-10-245-881-91	Sequence 91, Appl
82	793	13.9	2597	14	US-10-245-913-91	Sequence 91, Appl
83	793	13.9	2597	14	US-10-246-080-91	Sequence 91, Appl
84	793	13.9	2597	14	US-10-246-121-91	Sequence 91, Appl
85	793	13.9	2597	14	US-10-246-305-91	Sequence 91, Appl
86	793	13.9	2597	14	US-10-246-305-91	Sequence 91, Appl
87	793	13.9	2597	14	US-10-246-305-91	Sequence 91, Appl
88	793	13.9	2597	14	US-10-246-305-91	Sequence 91, Appl

89	793	13.9	2597	14	US-10-246-929-91	Sequence 91, Appl	C 162	20	0.4	482	10	US-09-918-995-20880	Sequence 20880, A
90	793	13.9	2597	14	US-10-247-036-91	Sequence 91, Appl	C 163	20	0.4	495	10	US-09-918-995-27967	Sequence 27967, A
91	793	13.9	2597	14	US-10-243-255-91	Sequence 91, Appl	C 164	20	0.4	508	15	US-10-027-632-286030	Sequence 286030, A
92	793	13.9	2597	14	US-10-245-810-91	Sequence 91, Appl	C 165	20	0.4	512	15	US-10-242-535A-17598	Sequence 17598, A
93	793	13.9	2597	14	US-10-245-910-91	Sequence 91, Appl	C 166	20	0.4	529	12	US-10-424-599-82975	Sequence 82975, A
94	793	13.9	2597	14	US-10-246-098-91	Sequence 91, Appl	C 167	20	0.4	595	15	US-10-027-632-286031	Sequence 286031, A
95	793	13.9	2597	14	US-10-237-966-91	Sequence 91, Appl	C 168	20	0.4	616	10	US-09-871-161-238	Sequence 238, App
96	793	13.9	2597	14	US-10-242-074-91	Sequence 91, Appl	C 169	20	0.4	700	9	US-09-880-107-2398	Sequence 3298, App
97	793	13.9	2597	14	US-10-242-505-91	Sequence 91, Appl	C 170	20	0.4	792	15	US-10-264-049-2020	Sequence 2020, App
98	793	13.9	2597	14	US-10-242-574-91	Sequence 91, Appl	C 171	20	0.4	1221	15	US-10-027-632-123804	Sequence 123804, A
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102	793	13.9	2597	14	US-10-243-431-91	Sequence 91, Appl	C 175	20	0.4	1536	9	US-10-037-270-702	Sequence 702, App
103	793	13.9	2597	14	US-10-245-164-91	Sequence 91, Appl	C 176	20	0.4	2522	14	US-10-117-722-702	Sequence 702, App
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106	793	13.9	2597	14	US-10-197-942-91	Sequence 91, Appl	C 179	20	0.4	6252	9	US-09-964-824A-313	Sequence 313, App
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253	19	0.3	2477	10	US-09-907-925-169	Sequence 169, App	326	19	0.3	2477	14	US-10-127-833A-331	Sequence 331, App
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258	19	0.3	2477	10	US-09-904-553-169	Sequence 169, App	331	19	0.3	2477	14	US-10-131-818A-331	Sequence 331, App
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685	19	0.3	2477	15	US-10-152-381-331	Sequence 331, App	758	18	0.3	400	13	US-10-099-926-1482	Sequence 1482, App
686	19	0.3	2477	15	US-10-152-400-331	Sequence 331, App	759	18	0.3	400	13	US-09-864-761-3100	Sequence 3180, App
687	19	0.3	2477	15	US-10-153-585-331	Sequence 331, App	760	18	0.3	400	13	US-10-424-599-2500	Sequence 2500, App
688	19	0.3	2477	15	US-10-157-780-331	Sequence 331, App	761	18	0.3	444	14	US-10-221-097-4	Sequence 4, App1
689	19	0.3	2477	15	US-10-157-800-331	Sequence 331, App	762	18	0.3	445	14	US-10-221-097-2	Sequence 2, App1
690	19	0.3	2477	15	US-10-157-801-331	Sequence 331, App	763	18	0.3	447	14	US-10-203-708-20	Sequence 20, App1
691	19	0.3	2477	15	US-10-157-802-331	Sequence 331, App	764	18	0.3	464	10	US-09-918-958-21601	Sequence 21601, A
692	19	0.3	2477	15	US-10-158-784-331	Sequence 331, App	765	18	0.3	468	15	US-10-115-479-7	Sequence 7, App1
693	19	0.3	2477	15	US-10-158-789-331	Sequence 331, App	766	18	0.3	470	9	US-09-864-761-5774	Sequence 5774, App
694	19	0.3	2477	15	US-10-158-791-331	Sequence 331, App	767	18	0.3	471	10	US-09-918-958-10117	Sequence 10117, A
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726	19	0.3	15856	10	US-09-764-891-8240	Sequence 8240, App	799	18	0.3	797	15	US-10-388-933-553	Sequence 553, App
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C 965 18 0.3 961 14 US-10-063-612-143 Sequence 143, App
C 966 18 0.3 961 14 US-10-063-615-143 Sequence 143, App
C 967 18 0.3 961 14 US-10-063-640-143 Sequence 143, App
C 968 18 0.3 961 14 US-10-063-642-143 Sequence 143, App
C 969 18 0.3 961 14 US-10-063-644-143 Sequence 143, App
C 970 18 0.3 961 14 US-10-063-649-143 Sequence 143, App
C 971 18 0.3 961 14 US-10-063-650-143 Sequence 143, App
C 972 18 0.3 961 14 US-10-063-652-143 Sequence 143, App
C 973 18 0.3 961 14 US-10-063-654-143 Sequence 143, App
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C 991 18 0.3 961 14 US-10-063-646-143 Sequence 143, App
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C 996 18 0.3 961 14 US-10-063-584-143 Sequence 143, App
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C 999 18 0.3 961 14 US-10-063-638-143 Sequence 143, App
C1000 18 0.3 961 14 US-10-063-666-143 Sequence 143, App
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## ALIGNMENTS

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RESULT 1
US-10-108-260A-802
; Sequence 802, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A.1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 802
; LENGTH: 3666
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-802
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Query Match 19.5%; Score 1108; DB 15; Length 3666;
Best Local Similarity 99.9%; Pred. 0;
Matches 1158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4527 TGGCAACAGCCCGAGGCTCCAGTAAGATCTCTCAACTGTGACACCATCACTCAGGTCA 4586
DB 1 TGGCAACAGCCCGAGGCTCCAGTAAGATCTCTCAACTGTGACACCATCACTCAGGTCA 60
QY 4587 GGAAGAGATTTGGATGCGATCTTCAAGATGCTTCCCAACCCGAGCCCAAGCTGC 4646
DB 61 GGAAGAGATTTGGATGCGATCTTCAAGATGCTTCCCAACCCGAGCCCAAGCTGC 120
QY 4647 AGATATGATCTTGAGTGGCGACAGAAAGTGGGGGAGAGATCTTGACAGATGAAGA 4706
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DB 121 AGATATGATCTTGAGTGGCGACAGAAAGTGGGGGAGAGATCTTGACAGATGAAGA 180
QY 4707 CATCACCAACCAATTTGAGATGATTTGAGAGGACCTGAAACACATGAGCCCACTACAGGT 4766
DB 181 CATCACCAACCAATTTGAGATGATTTGAGAGGACCTGAAACACATGAGCCCACTACAGGT 240
QY 4767 GCCAGATGATTCGGTGGTGGCATTTAGTGTCCAAAGAGTGAAGAGCTTATTAACGAGTGA 4826
DB 241 GCCAGATGATTCGGTGGTGGCATTTAGTGTCCAAAGAGTGAAGAGCTTATTAACGAGTGA 300
QY 4827 CAATCCACCGGTCTCCAGAGACCTCAGCAAGTAAATTTGAAACATGATCCGGTACACGGG 4886
DB 301 CAATCCACCGGTCTCCAGAGACCTCAGCAAGTAAATTTGAAACATGATCCGGTACACGGG 360
QY 4887 CACCCCGACAGCCTCCGCTCAGACGACCACTATGATCACTCTGACCTTGAGAGTGAAGT 4946
DB 361 CACCCCGACAGCCTCCGCTCAGACGACCACTATGATCACTCTGACCTTGAGAGTGAAGT 420
QY 4947 CAGATGTGACACTTGTGAAAGAACAGACGACGAGACCGAAGAGAGGGGACCGGGG 5006
DB 421 CAGATGTGACACTTGTGAAAGAACAGACGACGAGACCGAAGAGAGGGGACCGGGG 480
QY 5007 GAGCAAGATGATGTCTGAATCTTACCTGACCCGACTCTGACCACTTAAGGGACACTGCA 5066
DB 481 GAGCAAGATGATGTCTGAATCTTACCTGACCCGACTCTGACCACTTAAGGGACACTGCA 540
QY 5067 GAAATTTGGATGATGACCTCTTTAGACATCTTACGACAGGACACCGTGGCTTGGCCT 5126
DB 541 GAAATTTGGATGATGACCTCTTTAGACATCTTACGACAGGACACCGTGGCTTGGCCT 600
QY 5127 GCCCGTGGCATCAAGATGATGTTGACTCTGATGAGAGAGGCTGATTAACATGGCAT 5186
DB 601 GCCCGTGGCATCAAGATGATGTTGACTCTGATGAGAGAGGCTGATTAACATGGCAT 660
QY 5187 TCATGACCGGACGTCGCAATCTCTGAGAGAGCAATTCCTGACCTTGAAGTTTGGGT 5246
DB 661 TCATGACCGGACGTCGCAATCTCTGAGAGAGCAATTCCTGACCTTGAAGTTTGGGT 720
QY 5247 CAACATGATCAAGAACCCGAGTTGGTTGATCCATTAAGAACAGATCAACAGACG 5306
DB 721 CAACATGATCAAGAACCCGAGTTGGTTGATCCATTAAGAACAGATCAACAGACG 780
QY 5307 CTGCTCTCTGTGTGGTGGCTCAGACCTTCATGATGATCTTCTCTCCAGACCGGCT 5366
DB 781 CTGCTCTCTGTGTGGTGGCTCAGACCTTCATGATGATCTTCTCTCCAGACCGGCT 840
QY 5367 GGGCAAGAGATCGCCCTCCAAAGAGTGTATGCAAGAGACATCCAGGCTACAAGAA 5426
DB 841 GGGCAAGAGATCGCCCTCCAAAGAGTGTATGCAAGAGACATCCAGGCTACAAGAA 900
QY 5427 TTGGGTGAGAGGATATTACTCAGACATAGAGAGAGATCCAGGCTACGAGCAAGAT 5486
DB 901 TTGGGTGAGAGGATATTACTCAGACATAGAGAGAGATCCAGGCTACGAGCAAGAT 960
QY 5487 GAAAGCATACCTGCTGAGAGATCCCGGATGACATGAATGAGTTGAACACCACTGAGTGC 5546
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QY 5547 ACTCTCAGAGATCTTCTCTATGTGGGCAAAATACAGCGAGAGATCTTGAACCTTGA 5606
DB 1021 ACTCTCAGAGATCTTCTCTATGTGGGCAAAATACAGCGAGAGATCTTGAACCTTGA 1080
QY 5607 CACGATGACCAATGTGGGAGAGCAAACTGGGCTTCAAACTGAGAACATGCTAACCTCT 5666
DB 1081 CACGATGACCAATGTGGGAGAGCAAACTGGGCTTCAAACTGAGAACATGCTAACCTCT 1140
QY 5667 CATGAGCTTAGACAGCTGA 5685
DB 1141 CATGAGCTTAGACAGCTGA 1159
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RESULT 2
US-10-245-103-91
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Sequence 91, Application US/10245103  
Publication No. US20030068778A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C112  
CURRENT FILING DATE: 2002-09-17  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-103-91  
Query Match 13.9%; Score 793; DB 14; Length 2597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TGTAGAGGTGCCATTGGCTGTGAGCGAGTGGGTGAGTACCGCTGTGCGAGGCTGC 360  
Qy 939 CTAACCTGTCAAAGGCGGGGCGCTGTGGCAGACCCCTTGGATCCATCCAGATGATGA 998  
Db 361 CTAACCTGTCAAAGGCGGGGCGCTGTGGCAGACCCCTTGGATCCATCCAGATGATGA 420  
Qy 999 CCGCTCTTCAACCGCTCTTCTCAAAGGCGAGGCGGAAATGAATCCCTGATGAGTC 1058  
Db 421 CCGCTCTTCAACCGCTCTTCTCAAAGGCGAGGCGGAAATGAATCCCTGATGAGTC 480  
Qy 1059 GGCCTGTGCACTTCTCATCTTGAACGATTAATACCGCATTAAGAGCGGCTGCACTC 1118  
Db 481 GGCCTGTGCACTTCTCATCTTGAACGATTAATACCGCATTAAGAGCGGCTGCACTC 540  
Qy 1119 TTGTACCGGGGCGAGGGGCGAGCGTGGACCTGCGCTGCTGCAAGGTGAAGACATCCCTG 1178  
Db 541 TTGTACCGGGGCGAGGGGCGAGCGTGGACCTGCGCTGCTGCAAGGTGAAGACATCCCTG 600  
Qy 1179 CAGCAGTGGCTCTTAACCATTAACGATTAACCTTCTGTGCGCTGCAAGTATGCTCCCT 1238  
Db 601 CAGCAGTGGCTCTTAACCATTAACGATTAACCTTCTGTGCGCTGCAAGTATGCTCCCT 660  
Qy 1239 GGAAGTGTCCGACATGTGTCGTCGTAATCCGCTTCAAGAGCAGAGGACCGCATGAC 1298  
Db 661 GGAAGTGTCCGACATGTGTCGTCGTAATCCGCTTCAAGAGCAGAGGACCGCATGAC 720  
Qy 1299 GTCTGTCACTGATATGTCTACAGAACCACTCTGTGCGCTTGTGGCACCAGAAAGTG 1358  
Db 721 GTCTGTCACTGATATGTCTACAGAACCACTCTGTGCGCTTGTGGCACCAGAAAGTG 780  
Qy 1359 CAGCTGAAGAAG 1371  
Db 781 CAGCTGAAGAAG 793

RESULT 3  
US-10-245-107-91  
Sequence 91, Application US/10245107  
Publication No. US20030068779A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Baton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C171  
CURRENT FILING DATE: 2002-09-16  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801

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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/0090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/0096689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
LENGTH: 2597
TYPE: DNA
ORGANISM: Homo Sapien
US-10-245-107-91

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Query March	13.9%	Score 793	DB 14	Length 2597
Best Local Similarity	100.0%	Pred. No. 0		
Matches 793	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	579	CGAGTATTTTCCCAACCATCTCCAGCCGGAAACTACCAAGAACTCTGAGCGGATGGCAT	638
Db	1	CGAGTATTTTCCCAACCATCTCCAGCCGGAAACTACCAAGAACTCTGAGCGGATGGCAT	60
QY	639	GTTGCGGAGCTCTTCATGATGATGTTCTGTG3CCTCGATGATTTAGATCCCTTGGACAC	698
Db	61	GTTGCGGAGCTCTTCATGATGATGTTCTGTG3CCTCGATGATTTAGATCCCTTGGACAC	120
QY	699	CTTCACCATCATCCCGGATTTGGAATATCTACTATGTCTATGTTTTAGACAGTGGACACT	758
Db	121	CTTCACCATCATCCCGGATTTGGAATATCTACTATGTCTATGTTTTAGACAGTGGACACT	180
QY	759	TGCTCACTTTTGAACCCCTCAACCTGAGATGGTGTCTCCACAGGCTCCACACCAAGAA	818
Db	181	TGCTCACTTTTGAACCCCTCAACCTGAGATGGTGTCTCCACAGGCTCCACACCAAGAA	240
QY	819	GCAAGTGTATACATCCAGCTCTGTAGGCTTTGCAAGAGGACACAGCTTCAACTCTTA	878
Db	241	GCAAGTGTATACATCCAGCTCTGTAGGCTTTGCAAGAGGACACAGCTTCAACTCTTA	300
QY	879	TGTAGAGGTG3CCCATTTGCTGTAGACGAGTGG3GTGGAGTACCGGCTGTGTGAG3CTGC	938
Db	301	TGTAGAGGTG3CCCATTTGCTGTAGAGGAGTGG3GTGGAGTACCGGCTGTGTGAG3CTGC	360
QY	939	CTACCTGTCCAAAGCGG3GGCCGTCTTG3CAGACACCTTGAGTCCATCAATGATGA	998
Db	361	CTACCTGTCCAAAGCGG3GGCCGTCTTG3CAGACACCTTGAGTCCATCAATGATGA	420
QY	999	CTGTCTTCAACCGTCTTCTCCAG3GCCAGAGCGGAAAATGAAATCCTGTGATGATGC	1052
Db	421	CTGTCTTCAACCGTCTTCTCCAG3GCCAGAGCGGAAAATGAAATCCTGTGATGATGC	480
QY	1059	GGCCCTGTGATTTATCATCTGTAGGAGATTAATGACCGCATTAAGAGGCGGTGGAGTGC	1111
Db	481	GGCCCTGTGATTTATCATCTGTAGGAGATTAATGACCGCATTAAGAGGCGGTGGAGTGC	540
QY	1119	TTGTTAACCG3GGGAGAG3GACGCTG3ACCTG3CCTG3CTCAAG3TGAAGACATCCCTTG	1177
Db	541	TTGTTAACCG3GGGAGAG3GACGCTG3ACCTG3CCTG3CTCAAG3TGAAGACATCCCTTG	600
QY	1179	CAGAGATGGCCTCTTAACCATTTAGATGAATTACTTCTGTG3CCTG3CATGAAATGCTCCCT	1233
Db	601	CAGAGATGGCCTCTTAACCATTTAGATGAATTACTTCTGTG3CCTG3CATGAAATGCTCCCT	660
QY	1239	GGAGATGTCCGACATG3TGGTG3GAAATTC3CCTTCCAG3AGGACAG3GACCGCATGAC	1291
Db	661	GGAGATGTCCGACATG3TGGTG3GAAATTC3CCTTCCAG3AGGACAG3GACCGCATGAC	720
QY	1299	GTCGTGATCGCATATGTCTTAACAAGAACACTCTCTG3CCTTTGTG3GACACAAAGTGG	1355
Db	721	GTCGTGATCGCATATGTCTTAACAAGAACACTCTCTG3CCTTTGTG3G3GACACAAAGTGG	780
QY	1359	CAAGCTGAAAGAG 1371	
Db	781	CAAGCTGAAAGAG 793	

RESULT 4  
US-10-245-143-91  
; Sequence 91, Application US/10245143  
; Publication No. US20030068780A1  
; GENERAL INFORMATION:

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Query Match	13.9%	Score 793	DB 14	Length 2597
Best Local Similarly	100.0%	Pred. NO. 0		
Matches 793	0	Mismatches	0	Gaps 0

QY	579	CGAGATTTTCCCAACACATCTCCAGCCGAAACTGACCAAGAACTCTGAGGGGAAATGGCAT	638
Db	1	CGAGATTTTCCCAACATCTCCAGCCGAAACTGACCAAGAACTCTGAGGGGAAATGGCAT	60
QY	639	GTTGCGGAGCTCTTCATGATGATGATGTTGCGGCTCGATGATTAAGATCCCTTGGGACAC	698
Db	61	GTTGCGGAGCTCTTCATGATGATGATGTTGCGGCTCGATGATTAAGATCCCTTGGGACAC	120
QY	699	CTTACACATCACTCCCTGACTTTGATATCTATGTCATGTTGACATGGCAACTT	758
Db	121	CTTACACATCACTCCCTGACTTTGATATCTATGTCATGTTGACATGGCAACTT	180
QY	759	TGTCACATTTTGACCTTCGCAACTGAGATGCTGTCCACACAGGCTCCACACCAAGAA	818
Db	181	TGTCACATTTTGACCTTCGCAACTGAGATGCTGTCCACACAGGCTCCACACCAAGAA	240
QY	819	GCAGGTGATACATCCAAAGCTGTGAGGCTTTGCAGAAGGACACAGCTTCAACTCCTA	878

Db	241	GCAGGTGTATACATCCAACTGCTGTAGAGCTTTTGCAAGAGACACAGCTTCAACTCTTA	300
Qy	879	TGTAGAGGTGCCCATTTGCGTGTAGACGCAAGTGGGGTGGAGTACCGCTGTGCAGGCTGC	938
Db	301	TGTAGAGGTGCCCATTTGCGTGTAGACGCAAGTGGGGTGGAGTACCGCTGTGCAGGCTGC	380
Qy	939	CTACCTGTCCAAAGCGGGGGCCGTGTGGACGACCTTGGATGCCATCCAGATGATGA	998
Db	361	CTACCTGTCCAAAGCGGGGGCCGTGTGGACGACCTTGGATGCCATCCAGATGATGA	420
Qy	999	CTGTCTTTACCCGCTTCTCCAGGGCCAGAGCGGAAAAATGAAATCCTGTAGTAGTC	105
Db	421	CTGTCTTTACCCGCTTCTTCCTCCAGGGCCAGAGCGGAAAAATGAAATCCTGTAGTAGTC	480
Qy	1059	GGCCCTGTGTATCTTTATCTTTGAAGCAGATTAATACTGCATTTAAGAGGGCGTCGACGTC	111
Db	481	GGCCCTGTGTATCTTTATCTTTGAAGCAGATTAATACTGCATTTAAGAGGGCGTCGACGTC	540
Qy	1119	TTGTATCCGGGCGAGAGGACAGCTGGACCTGGCTGCGCTCAAGGTGAAGACATCCCTG	117
Db	541	TTGTATCCGGGCGAGAGGACAGCTGGACCTGGCTGCGCTCAAGGTGAAGACATCCCTG	600
Qy	1179	CAGCAGTGGCGCTTTTACATTGACGATPACTTTCTGTGGCTCGACATGAATGTTCCCT	123
Db	601	CAGCAGTGGCGCTTTTACATTGACGATPACTTTCTGTGGCTCGACATGAATGTTCCCT	660
Qy	1239	GGGAGTGTCCGACATGTCGCGTGAATTCGCTTCAAGAGACAGGACCGCATGAC	129
Db	661	GGGAGTGTCCGACATGTCGCGTGAATTCGCTTCAAGAGACAGGACCGCATGAC	720
Qy	1299	GTCGTGATGCAATATGTCTACAAAGACCACTCTTGCCCTTGTGGGACCAAAAGTGG	135
Db	721	GTCGTGATGCAATATGTCTACAAAGACCACTCTTGCCCTTGTGGGACCAAAAGTGG	780
Qy	1359	CAAGCTGAAGAG 1371	
Db	781	CAAGCTGAAGAG 793	

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; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-771-91

Query Match      13.9%; Score 793; DB 14; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCCAACATCTCCACCGGAAACGTACCAAGAACTCTAGGCGGATGCAT 638
DB 1 CGAGTATTTTCCCAACATCTCCACCGGAACTCAAGAACTCTAGGCGGATGCAT 60
QY 639 GTTCGCGTACCTCTTCATGATGATTGTTGTTGCTGCTCATGATTAAGATCCCTTGGACAC 698
DB 61 GTTCGCGTACCTCTTCATGATGATTGTTGTTGCTGCTCATGATTAAGATCCCTTGGACAC 120
QY 699 CTTCACCATCATCTCCCTGACTTTGATATCTACTANGTCTANGTCTTTTAGCATGGCATCTT 758
DB 121 CTTCACCATCATCTCCCTGACTTTGATATCTACTANGTCTANGTCTTTTAGCATGGCATCTT 180
QY 759 TGTCTACTTTTGAACCTCCCAACTGAGATGTTGTTCTCCACAGGCTCCACCAAGAAAGAA 818
DB 181 TGTCTACTTTTGAACCTCCCAACTGAGATGTTGTTCTCCACAGGCTCCACCAAGAAAGAA 240
QY 819 GCAGGTGTATTCATCCAAAGCTGTGAGGCTTTGCAAGAGAGACACAGCTTTCAAATCTCTA 878
DB 241 GCAGGTGTATTCATCCAAAGCTGTGAGGCTTTGCAAGAGAGACACAGCTTTCAAATCTCTA 300
QY 879 TGTAGAGGTGCCCATTTGCTGTGAGCGCAGTGGGATGGAATACCGCTGTGACAGGCTGC 938
DB 301 TGTAGAGGTGCCCATTTGCTGTGAGCGCAGTGGGATGGAATACCGCTGTGACAGGCTGC 360
QY 939 CTACCTGTCCAAAGCGGGGCGCTGTGAGGACCTTTGGAGTTCATCCAGATGATGA 998
DB 361 CTACCTGTCCAAAGCGGGGCGCTGTGAGGACCTTTGGAGTTCATCCAGATGATGA 420
QY 999 CCTGCTCTTACCGGCTTTCTCCAGGGGCGCAAGCGGAAATGAAATCCCTGATGAGTC 1058
DB 421 CCTGCTCTTACCGGCTTTCTCCAGGGGCGCAAGCGGAAATGAAATCCCTGATGAGTC 480
QY 1059 GGCCCTGTGATCTTTCATCTTTGAAGCAGATTAATGACCGCATTTAAGAGCGGCTGCACTC 1118
DB 481 GGCCCTGTGATCTTTCATCTTTGAAGCAGATTAATGACCGCATTTAAGAGCGGCTGCACTC 540
QY 1119 TTGTTATCCGGGGCGAGGGACAGCTGAGACTGTCGCTGCTCAAGGTGAAGACATCCCTGT 1178
DB 541 TTGTTATCCGGGGCGAGGGACAGCTGAGACTGTCGCTGCTCAAGGTGAAGACATCCCTGT 600
QY 1179 CAGCAGTGCCTCTTAAACATTTGACGATTAATCTTCTGAGGCTCTGACATGATGCTCCCT 1238
DB 601 CAGCAGTGCCTCTTAAACATTTGACGATTAATCTTCTGAGGCTCTGACATGATGCTCCCT 660
QY 1239 GGAAGTGTCCGACATGTGTGCTGAATTTCCGCTCTTCAAGGAGGACAGGACCGCATAC 1299
DB 661 GGAAGTGTCCGACATGTGTGCTGAATTTCCGCTCTTCAAGGAGGACAGGACCGCATAC 720
QY 1299 GTCTGTCATGTCATATGCTTCAAGAAACAATCTCTGAGCTTTTGTGGGACCAAAAGTG 1358
DB 721 GTCTGTCATGTCATATGCTTCAAGAAACAATCTCTGAGCTTTTGTGGGACCAAAAGTG 780
QY 1359 CAAGCTGAAGAG 1371

```

Db 781 CAAGCTGAAGAG 793

## RESULT 6

US-10-245-851-91  
Sequence 91, Application US/10245851  
Publication No. US20030068782A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Saton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C93  
CURRENT APPLICATION NUMBER: US/10/245,851  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-851-91

Query Match 13.9%; Score 793; DB 14; Length 2597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTCCACCATCTCCAGCCGGAACCTGAGCAAGAGTCTGAGCGCGAGTGCAT 638  
DB 1 CGAGTATTTCCACCATCTCCAGCCGGAACCTGAGCAAGAGTCTGAGCGCGAGTGCAT 60  
QY 639 GTTCGGGTAGTCTTCATGATGAGTTCGTCGTCGATGATTAAGATCCCTTCGACAC 698  
DB 61 GTTCGGGTAGTCTTCATGATGAGTTCGTCGTCGATGATTAAGATCCCTTCGACAC 120  
QY 699 CTTACCATCATCCCTGACCTTTGATCTACTATGCTCTAGTCTTTAGAGAGTGGCAACT 758  
DB 121 CTTACCATCATCCCTGACCTTTGATCTACTATGCTCTAGTCTTTAGAGAGTGGCAACT 180  
QY 759 TGTCTATTTTTCAGCCTCCAGCCTGAGTGTCTCCACAGGCTCCACCAAGGA 818  
DB 181 TGTCTATTTTTCAGCCTCCAGCCTGAGTGTCTCTCCACAGGCTCCACCAAGGA 240

QY 819 GCAGGTGATATCATCTCAACCTGCTGAGGCTTTGCAAGAGACACAGCTTCAATCCTA 878  
DB 241 GCAGGTGATATCATCTCAACCTGCTGAGGCTTTGCAAGAGACACAGCTTCAATCCTA 300  
QY 879 TGTAGAGGTGCCATGCTGCTGAGGAGTGGGCTGAGTACCGCTGCTCAGGCTGAC 938  
DB 301 TGTAGAGGTGCCATGCTGCTGAGGAGTGGGCTGAGTACCGCTGCTCAGGCTGAC 360  
QY 939 CTACCTGCTCAAGCGGCGGCTGCTGAGGAGACCTTGAAGTCCATCCGATGATGA 998  
DB 361 CTACCTGCTCAAGCGGCGGCTGCTGAGGAGACCTTGAAGTCCATCCGATGATGA 420  
QY 999 CCTGCTCTTACCGCTTCTTCCAGAGGCGGCAAGGCGGCAAGTCCCTGATGATGTC 1058  
DB 421 CCTGCTCTTACCGCTTCTTCCAGAGGCGGCAAGGCGGCAAGTCCCTGATGATGTC 480  
QY 1059 GSCCTGTGATCTTATCTTGAAGCATTAATGACCGCATTTAGAGCGGCTGATGTC 1118  
DB 481 GSCCTGTGATCTTATCTTGAAGCATTAATGACCGCATTTAGAGCGGCTGATGTC 540  
QY 1119 TTGTAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
DB 541 TTGTAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
QY 1179 CAGCAGTGGCTCTTACCATTTGACGATTAATGAGTCTGAGGAGGAGGAGGAGGAGG 1238  
DB 601 CAGCAGTGGCTCTTACCATTTGACGATTAATGAGTCTGAGGAGGAGGAGGAGGAGG 660  
QY 1239 GAGAGTGGCTCTTACCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1298  
DB 661 GAGAGTGGCTCTTACCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
QY 1299 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358  
DB 721 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 1359 CAAGCTGAAGAG 1371  
DB 781 CAAGCTGAAGAG 793

## RESULT 7

US-10-245-883-91  
Sequence 91, Application US/10245883  
Publication No. US20030068782A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Saton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C70  
CURRENT APPLICATION NUMBER: US/10/245,883  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689  
 ; PRIOR FILING DATE: 1998-06-25  
 ; Remaining Prior Application data removed - See File Wrapper or PAM.  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SEQ ID NO 91  
 ; LENGTH: 2597  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-245-883-91

Query March 13.9%; Score 793; DB 14; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCGACCATCTCCAGCCGGAATGACCAAGAACTGTGAGCGGATGGCAT 638  
 DB 1 CGAGTATTTTCCGACCATCTCCAGCCGGAATGACCAAGAACTGTGAGCGGATGGCAT 60  
 QY 639 GTTCGCGTACGCTCTTCATATAGATGTTGCGGCTCGATGATTAATCCCTTCGGACAC 698  
 DB 61 GTTCGCGTACGCTCTTCATATAGATGTTGCGGCTCGATGATTAATCCCTTCGGACAC 120  
 QY 699 CTTGACCATCATCCCTGACTTTGATATCTATCTATGTTTGAAGATGGCACTT 758  
 DB 121 CTTGACCATCATCCCTGACTTTGATATCTATCTATGTTTGAAGATGGCACTT 180  
 QY 759 TGTGTACTTTTGAACCTCCAGCTGAGATGTTGTTCCACCGGCTCCACCAAGAGA 818  
 DB 181 TGTGTACTTTTGAACCTCCAGCTGAGATGTTGTTCCACCGGCTCCACCAAGAGA 240  
 QY 819 GCAAGTATATATATCAAGCTGCTGAGGCTTTGCAAGAGACACAGCCTTCACTCTA 878  
 DB 241 GCAAGTATATATATCAAGCTGCTGAGGCTTTGCAAGAGACACAGCCTTCACTCTA 300  
 QY 879 TGTGAGAGTGGCCATTGGCTGTGAGCCGATGGGGTGGAGTATCCGCTGTGAGGCTGC 938  
 DB 301 TGTGAGAGTGGCCATTGGCTGTGAGCCGATGGGGTGGAGTATCCGCTGTGAGGCTGC 360  
 QY 939 CTACCTGTCCAAAGCGGGGCGCGCTTGGCAAGACCTTGGAGTCATCCAGATGATGA 998  
 DB 361 CTACCTGTCCAAAGCGGGGCGCGCTTGGCAAGACCTTGGAGTCATCCAGATGATGA 420  
 QY 999 CTGCTCTTCAACGCTCTTCTCCAAAGGCGCAAGCGGAAATTAATCCCTGATGATGC 1058  
 DB 421 CTGCTCTTCAACGCTCTTCTCCAAAGGCGCAAGCGGAAATTAATCCCTGATGATGC 480  
 QY 1059 GGCCCTGTGATCTTCACTTCTTGAAGCAGATTAATGACCGATTAAGAGGGGCTGAGTC 1118  
 DB 481 GGCCCTGTGATCTTCACTTCTTGAAGCAGATTAATGACCGATTAAGAGGGGCTGAGTC 540  
 QY 1119 TTGTATCCGGGCGAGGCGACGCTGACCTGGCCTGGCTCAAGGTGAAGACATCCCTTG 1178  
 DB 541 TTGTATCCGGGCGAGGCGACGCTGACCTGGCCTGGCTCAAGGTGAAGACATCCCTTG 600  
 QY 1179 CAGAGAGCGCTCTTAACTTAAGCATTAATCTTGTGGCTGAGATCAATGCTCCCT 1238  
 DB 601 CAGAGAGCGCTCTTAACTTAAGCATTAATCTTGTGGCTGAGATCAATGCTCCCT 660  
 QY 1239 GGAAGTGTCCGACATGTGTGGGTGAATTCGCTTTCAGGAGACAGGACCGCATGAC 1298  
 DB 661 GGAAGTGTCCGACATGTGTGGGTGAATTCGCTTTCAGGAGACAGGACCGCATGAC 720  
 QY 1299 GTCTGTATGGCAATATCTTAAGAAACCACTCTGCGCTTTGTGGGCGCAAAAGTGG 1358

DB 721 GTCTGTATCCGATATGCTTACAGAACCACTCTCTGGCCTTTGTGGGCAACCAAGTGG 780  
 QY 1359 CAAGCTGAAGAG 1371  
 DB 781 CAAGCTGAAGAG 793

RESULT 8  
 US-10-237-535-91  
 ; Sequence 91, Application US/10237535  
 ; Publication No. US20030073188A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Balcon, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gutney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe  
 ; APPLICANT: Matanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Pong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3630R1C3  
 ; CURRENT APPLICATION NUMBER: US/10/237,535  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689  
 ; PRIOR FILING DATE: 1998-06-25  
 ; PRIOR APPLICATION NUMBER: 60/091358  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/099803  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/106932  
 ; PRIOR FILING DATE: 1998-11-03  
 ; PRIOR APPLICATION NUMBER: 60/115554  
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 ; PRIOR APPLICATION NUMBER: 60/119342  
 ; PRIOR FILING DATE: 1999-02-09  
 ; PRIOR APPLICATION NUMBER: 60/123957  
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 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/135725  
 ; PRIOR FILING DATE: 1999-05-25



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 PRIOR FILING DATE: 1999-05-25  
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 PRIOR FILING DATE: 1999-05-25  
 PRIOR APPLICATION NUMBER: 60/138385  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: 60/140653  
 PRIOR FILING DATE: 1999-06-22  
 PRIOR APPLICATION NUMBER: 60/141037  
 PRIOR FILING DATE: 1999-06-23  
 PRIOR APPLICATION NUMBER: 60/144732  
 PRIOR FILING DATE: 1999-07-20  
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 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: 60/146222  
 PRIOR FILING DATE: 1999-07-28  
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 PRIOR FILING DATE: 1999-08-03  
 PRIOR APPLICATION NUMBER: 60/148188  
 PRIOR FILING DATE: 1999-08-10  
 PRIOR APPLICATION NUMBER: 60/148513  
 PRIOR FILING DATE: 1999-08-12  
 PRIOR APPLICATION NUMBER: 60/149327  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/149395  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/150114  
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 PRIOR APPLICATION NUMBER: 60/262150  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: 60/264395  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 60/266421  
 PRIOR FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: 60/267623  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/274399  
 PRIOR FILING DATE: 2001-03-09  
 PRIOR APPLICATION NUMBER: 60/280982  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/282129  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/282199  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/290589  
 PRIOR FILING DATE: 2001-05-09  
 PRIOR APPLICATION NUMBER: 60/280997  
 PRIOR FILING DATE: 1998-11-19  
 PRIOR APPLICATION NUMBER: 60/267213  
 PRIOR FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 60/380137  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 60/380138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 60/403297  
 PRIOR FILING DATE: 1999-10-18  
 PRIOR APPLICATION NUMBER: 60/423741  
 PRIOR FILING DATE: 1999-11-10  
 PRIOR APPLICATION NUMBER: 60/709238  
 PRIOR FILING DATE: 2000-11-08  
 PRIOR APPLICATION NUMBER: 60/802706  
 PRIOR FILING DATE: 2001-03-09  
 PRIOR APPLICATION NUMBER: 60/872035  
 PRIOR FILING DATE: 2001-06-01  
 PRIOR APPLICATION NUMBER: 60/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/924419  
 PRIOR FILING DATE: 2001-08-06  
 PRIOR APPLICATION NUMBER: 60/927796  
 PRIOR FILING DATE: 2001-08-09  
 PRIOR APPLICATION NUMBER: 60/929404  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: 60/931836  
 PRIOR FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: 60/941992  
 PRIOR FILING DATE: 2001-08-28  
 PRIOR APPLICATION NUMBER: 60/946374  
 PRIOR FILING DATE: 2001-09-04  
 PRIOR APPLICATION NUMBER: 60/001054  
 PRIOR FILING DATE: 2001-11-30  
 PRIOR APPLICATION NUMBER: 60/052586  
 PRIOR FILING DATE: 2002-01-15  
 PRIOR APPLICATION NUMBER: 60/081056  
 PRIOR FILING DATE: 2002-02-20  
 PRIOR APPLICATION NUMBER: 60/119480  
 PRIOR FILING DATE: 2002-04-09

Query Match 13.9%; Score 793; DB 14; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCGACATCTTCACCGGAATGACCAAGAACTCTGAGGCGATGGCAT 638  
 DB 1 CGAGTATTTTCCGACATCTTCACCGGAATGACCAAGAACTCTGAGGCGATGGCAT 60  
 QY 639 GTTCGCTACGTCCTTCATGATGATGCTGCGCTCGATGATTAAGATCCCTTCGACAC 698



PRIOR APPLICATION NUMBER: 60/149327  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/149395  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/150114  
 PRIOR FILING DATE: 1999-08-20  
 PRIOR APPLICATION NUMBER: 60/151700  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: 60/151734  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: 60/162506  
 PRIOR FILING DATE: 1999-10-29  
 PRIOR APPLICATION NUMBER: 60/170262  
 PRIOR FILING DATE: 1999-12-09  
 PRIOR APPLICATION NUMBER: 60/177118  
 PRIOR FILING DATE: 2000-01-20  
 PRIOR APPLICATION NUMBER: 60/179851  
 PRIOR FILING DATE: 2000-02-02  
 PRIOR APPLICATION NUMBER: 60/180921  
 PRIOR FILING DATE: 2000-02-08  
 PRIOR APPLICATION NUMBER: 60/187202  
 PRIOR FILING DATE: 2000-03-03  
 PRIOR APPLICATION NUMBER: 60/198587  
 PRIOR FILING DATE: 2000-04-16  
 PRIOR APPLICATION NUMBER: 60/199614  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: 60/206330  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/206568  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/209832  
 PRIOR FILING DATE: 2000-06-05  
 PRIOR APPLICATION NUMBER: 60/218371  
 PRIOR FILING DATE: 2000-07-13  
 PRIOR APPLICATION NUMBER: 60/222695  
 PRIOR FILING DATE: 2000-08-02  
 PRIOR APPLICATION NUMBER: 60/229896  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/230621  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/232887  
 PRIOR FILING DATE: 2000-09-15  
 PRIOR APPLICATION NUMBER: 60/235147  
 PRIOR FILING DATE: 2000-09-22  
 PRIOR APPLICATION NUMBER: 60/261878  
 PRIOR FILING DATE: 2001-01-12  
 PRIOR APPLICATION NUMBER: 60/261910  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: 60/261939  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: 60/262150  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: 60/264395  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 60/264421  
 PRIOR FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: 60/267623  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/274399  
 PRIOR FILING DATE: 2001-03-09  
 PRIOR APPLICATION NUMBER: 60/280982  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/282129  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/282199  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/290589  
 PRIOR FILING DATE: 2001-05-09  
 PRIOR APPLICATION NUMBER: 09/180997  
 PRIOR FILING DATE: 1998-11-19  
 PRIOR APPLICATION NUMBER: 09/267213  
 PRIOR FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 09/380137

PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/403297  
 PRIOR FILING DATE: 1999-10-18  
 PRIOR APPLICATION NUMBER: 09/423741  
 PRIOR FILING DATE: 1999-11-10  
 PRIOR APPLICATION NUMBER: 09/709238  
 PRIOR FILING DATE: 2000-11-08  
 PRIOR APPLICATION NUMBER: 09/802706  
 PRIOR FILING DATE: 2001-03-09  
 PRIOR APPLICATION NUMBER: 09/872035  
 PRIOR FILING DATE: 2001-06-01  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 09/924419  
 PRIOR FILING DATE: 2001-08-06  
 PRIOR APPLICATION NUMBER: 09/927796  
 PRIOR FILING DATE: 2001-08-09  
 PRIOR APPLICATION NUMBER: 09/929404  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: 09/931836  
 PRIOR FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: 09/941992  
 PRIOR FILING DATE: 2001-08-28  
 PRIOR APPLICATION NUMBER: 09/946374  
 PRIOR FILING DATE: 2001-09-04  
 PRIOR APPLICATION NUMBER: 10/001054  
 PRIOR FILING DATE: 2001-11-30  
 PRIOR APPLICATION NUMBER: 10/052586  
 PRIOR FILING DATE: 2002-01-15  
 PRIOR APPLICATION NUMBER: 10/081056  
 PRIOR FILING DATE: 2002-02-20  
 PRIOR APPLICATION NUMBER: 10/119480  
 PRIOR FILING DATE: 2002-04-09

Query Match 13.9%; Score 793; DB 14; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCACATCTCCAGCCGGAAGTGAAGAACTGTGAGGGGATGGCAT 638  
 DB 1 CGAGTATTTTCCACATCTCCAGCCGGAAGTGAAGAACTGTGAGGGGATGGCAT 60  
 QY 639 GTTCGGTACGTCTTCATGATGATGTCGTGCTCGATGATTAATCCCTTGGACAC 698  
 DB 61 GTTCGGTACGTCTTCATGATGATGTCGTGCTCGATGATTAATCCCTTGGACAC 120  
 QY 699 CTTACACATCATCCCTGATCTTTGATATCTATGTTATGTTTATGAGTGGCACTT 758  
 DB 121 CTTACACATCATCCCTGATCTTTGATATCTATGTTATGTTTATGAGTGGCACTT 180  
 QY 759 TGTCTACTTTTGAACCTCCAACTGAGATGATGTCCTCCACAGGCTCCACCAAGA 818  
 DB 181 TGTCTACTTTTGAACCTCCAACTGAGATGATGTCCTCCACAGGCTCCACCAAGA 240  
 QY 819 GAGGTGTATACATCAAGCTGTGAGCTTTGCAAGAGGACACACCTTTAACTCTTA 878  
 DB 241 GAGGTGTATACATCAAGCTGTGAGCTTTGCAAGAGGACACACCTTTAACTCTTA 300  
 QY 879 TGTAGAAGTGCATTTGGCTGTGAGGAGGAGTGGGTGAGTACCGCTCTGAGAGCTGC 938  
 DB 301 TGTAGAAGTGCATTTGGCTGTGAGGAGGAGTGGGTGAGTACCGCTCTGAGAGCTGC 360  
 QY 939 CTACTGTCCAAAGCGGGGGCGTGTGTTGGACAGACCTTTGAGTCCATCCAGATGATA 998  
 DB 361 CTACTGTCCAAAGCGGGGGCGTGTGTTGGACAGACCTTTGAGTCCATCCAGATGATA 420  
 QY 999 CCGTCTTACCCGCTCTTCTCCAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1058  
 DB 421 CCGTCTTACCCGCTCTTCTCCAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 QY 1059 GGCCCTGTGATCTTCACTTGAAGCAGATTAATGACCGCATTAAGAGAGCGGTGAGTIC 1118

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Db      481 GGGCCCTGACATCTTCACTTGAAGACATTAATGAACGACATTAAGAGCGGGCTGCAGCTC 540
Qy      1119 TTGTTACCGGGGCGAGGCGACGCTGACCTGCGCTGCTCAAGGTGAAGACATCCCTG 1178
Db      541 TTGTTACCGGGGCGAGGCGACGCTGACCTGCGCTGCTCAAGGTGAAGACATCCCTG 600
Qy      1179 CAGCAGTGGGCTCTTAACCATTTGAGAGATACTTCTGTGGCTTGAACATGAATGCTCCCT 1238
Db      601 CAGCAGTGGGCTCTTAACCATTTGAGAGATACTTCTGTGGCTTGAACATGAATGCTCCCT 660
Qy      1239 GGGAGTGTCCGACATGATGTCGTCGAATTCCTGCTTCAAGAGACAGGAGCCGATGAC 1298
Db      661 GGGAGTGTCCGACATGATGTCGTCGAATTCCTGCTTCAAGAGACAGGAGCCGATGAC 720
Qy      1299 GTCTGTCAATGCAATATGTCATACAGAACCACTCTGTGGCTTTGTGGGACCAAAAGTGG 1358
Db      721 GTCTGTCAATGCAATATGTCATACAGAACCACTCTGTGGCTTTGTGGGACCAAAAGTGG 780
Qy      1359 CAAGCTGAAGAAG 1371
Db      781 CAAGCTGAAGAAG 793

RESULT 10
US-10-238-283-91
; Sequence 91, Application US/10238283
; Publication No. US20030073190A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Collin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C15
CURRENT APPLICATION NUMBER: US/10/238,283
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065927
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
LENGTH: 2597
TYPE: DNA
ORGANISM: Homo Sapien
US-10-238-283-91

```

```

Query Match      13.9%; Score 793; DB 14; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      579 CGAGTATTTTCCCAACCATCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGGATGSCAT 638
Db      1 CGAGTATTTTCCCAACCATCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGGATGSCAT 60
Qy      639 GTTCGGGTACGTCTTCATGATGAGTTCGTGGCTTCGATGATTAAGATCCCTTGGACAC 698
Db      61 GTTCGGGTACGTCTTCATGATGAGTTCGTGGCTTCGATGATTAAGATCCCTTGGACAC 120
Qy      699 CTTACCATCATACCCCTGACCTTGATATCTACTATGTCATATGTTTGAAGTGGCACTT 758
Db      121 CTTACCATCATACCCCTGACCTTGATATCTACTATGTCATATGTTTGAAGTGGCACTT 180
Qy      759 TGTCTACTTTTGAACCTTCGAACCTGAGATGCTGTCTCCACAGGCTCCACCAAGGA 818
Db      181 TGTCTACTTTTGAACCTTCGAACCTGAGATGCTGTCTCCACAGGCTCCACCAAGGA 240
Qy      819 GCAGGTATATACATCCAGCTGTGAGGCTTGAAGAGACACAGCTTCACTCTTA 878
Db      241 GCAGGTATATACATCCAGCTGTGAGGCTTGAAGAGACACAGCTTCACTCTTA 300
Qy      879 TGTAGAGTGGCCATTTGCTGTGAGGCGAGTGGGTGAATACCGCTGCTGCAAGCTGC 938
Db      301 TGTAGAGTGGCCATTTGCTGTGAGGCGAGTGGGTGAATACCGCTGCTGCAAGCTGC 360
Qy      939 CTACCTGTCCAAAGCGGGGCGGCTGTGGCAGAGACCTTGAAGTCCATCCAGATGATGA 998
Db      361 CTACCTGTCCAAAGCGGGGCGGCTGTGGCAGAGACCTTGAAGTCCATCCAGATGATGA 420
Qy      999 CTGCTCTTCAACCGCTTCTTCCAGAGGCGGCAAGAAATGAATCCCTGATGATGC 1058
Db      421 CTGCTCTTCAACCGCTTCTTCCAGAGGCGGCAAGAAATGAATCCCTGATGATGC 480
Qy      1059 GGGCTGTGATTTTATCTTGAAGGATTAATGACCGCATTAAGAGACGGCTGAGTC 1118
Db      481 GGGCTGTGATTTTATCTTGAAGGATTAATGACCGCATTAAGAGACGGCTGAGTC 540
Qy      1119 TTGTACCGGGGCGAGGCGACGCTGACCTGCGCTCAAGGTGAAGACATCCCTG 1178
Db      541 TTGTACCGGGGCGAGGCGACGCTGACCTGCGCTCAAGGTGAAGACATCCCTG 600
Qy      1179 CAGCAGTGGGCTCTTAACCATTTGAGAGATACTTCTGTGGCTTGAACATGAATGCTCCCT 1238
Db      601 CAGCAGTGGGCTCTTAACCATTTGAGAGATACTTCTGTGGCTTGAACATGAATGCTCCCT 660
Qy      1239 GGGAGTGTCCGACATGATGTCGTCGAATTCCTGCTTCAAGAGACAGGAGCCGATGAC 1298
Db      661 GGGAGTGTCCGACATGATGTCGTCGAATTCCTGCTTCAAGAGACAGGAGCCGATGAC 720
Qy      1299 GTCTGTCAATGCAATATGTCATACAGAACCACTCTGTGGCTTTGTGGGACCAAAAGTGG 1358
Db      721 GTCTGTCAATGCAATATGTCATACAGAACCACTCTGTGGCTTTGTGGGACCAAAAGTGG 780
Qy      1359 CAAGCTGAAGAAG 1371
Db      781 CAAGCTGAAGAAG 793

RESULT 11
US-10-238-370-91
; Sequence 91, Application US/10238370
; Publication No. US20030073191A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
US-10-238-370-91

```

```

APPLICANT: Smith,Victoria
APPLICANT: Stephan,Jean-Philippe
APPLICANT: Matanbe,Colin
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
APPLICANT: Fong,Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C10
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US/10/238,370
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
LENGTH: 2597
TYPE: DNA
ORGANISM: Homo Sapien
US-10-238-370-91

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```

Query Match      13.9% Score 793; DB 14; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 793; Conservative 0;
579 CGAGTATTTCCACCATCTCCAGCCGGAACCTGACCAAGAACTCTGAGCGGATGGCAT 638
1 CGAGTATTTCCACCATCTCCAGCCGGAACCTGACCAAGAACTCTGAGCGGATGGCAT 60
639 GTTCCGCTACGCTTCCATGATGATTTGGCCCTCCGATGATTAAGATCCCTTGGGACAC 698
61 GTTCCGCTACGCTTCCATGATGATTTGGCCCTCCGATGATTAAGATCCCTTGGGACAC 120
699 CTTCAACCATCATCCCTGACTTGTATATCTATGTTAGTGGTGGCACTT 758
121 CTTCAACCATCATCCCTGACTTGTATATCTATGTTAGTGGTGGCACTT 180
759 TGTCTACTTTTGGACCTTCCAACTGATGATGTTGCTCCACAGGCTCCACCAAGGA 818
181 TGTCTACTTTTGGACCTTCCAACTGATGATGTTGCTCCACAGGCTCCACCAAGGA 240
819 GCAGGTGTATACATCCAAAGCTGTAGAGGCTTTGCAAGGAGGACACAGGCTTCACTCTTA 878
241 GCAGGTGTATACATCCAAAGCTGTAGAGGCTTTGCAAGGAGGACACAGGCTTCACTCTTA 300
879 TGTAGAGGTGCCCATTTGGCTGTAGAGGAGCAGTGGGGTGAAGTACCCGCTTGGCAGGCTGC 938
301 TGTAGAGGTGCCCATTTGGCTGTAGAGGAGCAGTGGGGTGAAGTACCCGCTTGGCAGGCTGC 360
939 CTACCTGTCCAAAGCGGGGCGGTGTTGGCAGAGCCCTTGGAGTCCATCCAGATGATGA 998
361 CTACCTGTCCAAAGCGGGGCGGTGTTGGCAGAGCCCTTGGAGTCCATCCAGATGATGA 420
999 CCTGCTCTTACCGCTTCTTCCAAAGGCGCAAGGCGGAAATGAAATCCCTGGATGATGC 1058

```

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Db 421 CCTGCTCTTACCGCTTCTTCCAAAGGCGCAAGGCGGAAATGAAATCCCTGGATGATGC 480
Qy 1059 GGGCCCTGTGATCTTCACTTCTTGAAGCAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 1118
Db 481 GGGCCCTGTGATCTTCACTTCTTGAAGCAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 540
Qy 1119 TTGTTACCGGGGCGAGGGCAGCTGAGCTGGCTGGCTCAAGGTGAAGGACATCCCTG 1178
Db 541 TTGTTACCGGGGCGAGGGCAGCTGAGCTGGCTGGCTCAAGGTGAAGGACATCCCTG 600
Qy 1179 CAGCAGTGCCTCTTAACCATTTGACATGATTACTTGTGGCTGTGACATGAATGCTCCCT 1238
Db 601 CAGCAGTGCCTCTTAACCATTTGACATGATTACTTGTGGCTGTGACATGAATGCTCCCT 660
Qy 1239 GGGAGTGTCCGACATGTCGTCGATGAAATCCGCTCTTACCGAGAGACGGGACCGCATGAC 1298
Db 661 GGGAGTGTCCGACATGTCGTCGATGAAATCCGCTCTTACCGAGAGACGGGACCGCATGAC 720
Qy 1299 GTCTGTCAATCGCATATGTTCTACAGAACCACTCTTGGCTTTGTGGGACCAAAAGTGG 1358
Db 721 GTCTGTCAATCGCATATGTTCTACAGAACCACTCTTGGCTTTGTGGGACCAAAAGTGG 780
Qy 1359 CAAGCTGAAGAG 1371
Db 781 CAAGCTGAAGAG 793

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RESULT 12
US-10-245-055-91
Sequence 91, Application US/10245055
Publication No. US20030073192A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Ealon, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, U. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Matanbe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C8
CURRENT APPLICATION NUMBER: US/10/245,055
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
LENGTH: 2597

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-055-91
Query Match      13.9%; Score 793; DB 14; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCCAACCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGATGATGAT 638
DB 1 CGAGTATTTTCCCAACCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGATGATGAT 60
QY 639 GTTCGCGTACGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 698
DB 61 GTTCGCGTACGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 699 CTTCACCATCATCCCTGATCTTGAATATCTATGATGATGATGATGATGATGATGAT 758
DB 121 CTTCACCATCATCCCTGATCTTGAATATCTATGATGATGATGATGATGATGATGAT 180
QY 759 TGTCTACTTTTGAACCTCCCAACCTGAGATGATGATGATGATGATGATGATGATGAT 818
DB 181 TGTCTACTTTTGAACCTCCCAACCTGAGATGATGATGATGATGATGATGATGATGAT 240
QY 819 GCAAGGTATATACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 878
DB 241 GCAAGGTATATACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 879 TGTAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
DB 301 TGTAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 939 CTACCTGTCCAAAGCGGGGGCGGTCTTGGAGAGACCTTGGAGTCCATCCAGTATGATGA 998
DB 361 CTACCTGTCCAAAGCGGGGGCGGTCTTGGAGAGACCTTGGAGTCCATCCAGTATGATGA 420
QY 999 CCTGCTCTTCAACCGCTCTTCCAGAGGGCCAGAAAGGAAATGAAATCCCTGATGATGAT 1058
DB 421 CCTGCTCTTCAACCGCTCTTCCAGAGGGCCAGAAAGGAAATGAAATCCCTGATGATGAT 480
QY 1059 GGCCTGTGATCATCTTCAATCTTGAAGCAATTAATGACCGCATTTAAGAGCGGCTGCACTC 1118
DB 481 GGCCTGTGATCATCTTCAATCTTGAAGCAATTAATGACCGCATTTAAGAGCGGCTGCACTC 540
QY 1119 TTGTTACCGGGGGCGAGGGGACCTGAGACCTGCGCTGCAAGGTGAAGAGACATCCCTG 1178
DB 541 TTGTTACCGGGGGCGAGGGGACCTGAGACCTGCGCTGCAAGGTGAAGAGACATCCCTG 600
QY 1179 CAGCAGTGGGCTCTTAACCATTTAGCATTAATCTTGTGCGCTGAGCATGAATGCTCCCT 1238
DB 601 CAGCAGTGGGCTCTTAACCATTTAGCATTAATCTTGTGCGCTGAGCATGAATGCTCCCT 660
QY 1239 GGAAGTGTCCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
DB 661 GGAAGTGTCCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 1299 GTCTGTATCGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
DB 721 GTCTGTATCGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 1359 CAAGCTGAAGAAG 1371
DB 781 CAAGCTGAAGAAG 793

```

```

; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C72
; CURRENT APPLICATION NUMBER: US/10/245,147
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-147-91
Query Match      13.9%; Score 793; DB 14; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCCAACCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGATGATGAT 638
DB 1 CGAGTATTTTCCCAACCTCCAGCCGGAACCTGACCAAGAACTCTGAGGCGATGATGAT 60
QY 639 GTTCGCGTACGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 698
DB 61 GTTCGCGTACGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 699 CTTCACCATCATCCCTGATCTTGAATATCTATGATGATGATGATGATGATGATGAT 758
DB 121 CTTCACCATCATCCCTGATCTTGAATATCTATGATGATGATGATGATGATGATGAT 180
QY 759 TGTCTACTTTTGAACCTCCCAACCTGAGATGATGATGATGATGATGATGATGATGAT 818
DB 181 TGTCTACTTTTGAACCTCCCAACCTGAGATGATGATGATGATGATGATGATGATGAT 240
QY 819 GCAAGGTATATACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 878
DB 241 GCAAGGTATATACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 879 TGTAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
DB 301 TGTAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 939 CTACCTGTCCAAAGCGGGGGCGGTCTTGGAGAGACCTTGGAGTCCATCCAGTATGATGA 998
DB 361 CTACCTGTCCAAAGCGGGGGCGGTCTTGGAGAGACCTTGGAGTCCATCCAGTATGATGA 420

```

QY 999 CTTGCTTTGACCGCTCTTCTCCAGAGGCCGAGAAATGAAATCCCTGATGAGTC 1058  
Db 421 CTTGCTTTGACCGCTCTTCTCCAGAGGCCGAGAAATGAAATCCCTGATGAGTC 480  
QY 1059 GGCCCTGTCATCTTCACTTTGAAGCAGATAATGACCGCATTAAGAGCGCTGACATC 1118  
Db 481 GGCCCTGTCATCTTCACTTTGAAGCAGATAATGACCGCATTAAGAGCGCTGACATC 540  
QY 1119 TTGTTACCGGAGCGAGGACAGCTGACCTGCGCTGCTCAAGTGAAGACATCCCTCG 1178  
Db 541 TTGTTACCGGAGCGAGGACAGCTGACCTGCGCTGCTCAAGTGAAGACATCCCTCG 600  
QY 1179 CAGCAGTGCCTCTTAACCATTTGACATCTTGTGAGCTGACATGATGCTCCCT 1238  
Db 601 CAGCAGTGCCTCTTAACCATTTGACATCTTGTGAGCTGACATGATGCTCCCT 660  
QY 1239 GGGAGTGTCCGACATGTGTGCGTGAATTCCTGCTTCAAGAGACAGGACCGCATGAC 1298  
Db 661 GGGAGTGTCCGACATGTGTGCGTGAATTCCTGCTTCAAGAGACAGGACCGCATGAC 720  
QY 1299 GTCTGTATGSCATATGCTTCAAGAACCACTCTGCTGCTTGTGAGGACCAAAAGTGG 1358  
Db 721 GTCTGTATGSCATATGCTTCAAGAACCACTCTGCTGCTTGTGAGGACCAAAAGTGG 780  
QY 1359 CAAGCTGAAGAG 1371  
Db 781 CAAGCTGAAGAG 793

RESULT 14  
US-10-245-730-91  
; Sequence 91, Application US/10245730  
; Publication No. US20030073194A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eason, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Warabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C85  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/10/245,730  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 91  
; LENGTH: 2597  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-245-730-91

Query Match 13.9%; Score 793; DB 14; Length 2597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCCAACATCTTCCAGCCGAGAACTGACCAAGAACTGAGGCGGATGGCAT 638  
Db 1 CGAGTATTTTCCCAACATCTTCCAGCCGAGAACTGACCAAGAACTGAGGCGGATGGCAT 60  
QY 639 GTTCCGTCAGCTTCTTCATGATGAGTTGCGGCTGCGATTAAGATCCCTTGGACAC 698  
Db 61 GTTCCGTCAGCTTCTTCATGATGAGTTGCGGCTGCGATTAAGATCCCTTGGACAC 120  
QY 699 CTTACCATCATTCCTGACTTTGATATCTACTATGCTATGCTTTAGAGTGGCACTT 758  
Db 121 CTTACCATCATTCCTGACTTTGATATCTACTATGCTATGCTTTAGAGTGGCACTT 180  
QY 759 TGTCTACTTTTGAACCTCCCACTGAGATGATGCTCTCCACAGAGCTCCACCAAGGA 818  
Db 181 TGTCTACTTTTGAACCTCCCACTGAGATGATGCTCTCCACAGAGCTCCACCAAGGA 240  
QY 819 GCAGGTGATATCATCCAAAGCTGTGAGGCTTTGCAAGAGACACAGCTTCAACTCTTA 878  
Db 241 GCAGGTGATATCATCCAAAGCTGTGAGGCTTTGCAAGAGACACAGCTTCAACTCTTA 300  
QY 879 TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGTGACAGCTGC 938  
Db 301 TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGTGACAGCTGC 360  
QY 939 CTACCTGTCCAAAGCGGGGCGCTGTGAGGACCTTTGAGTCCATCCAGATGATGA 998  
Db 361 CTACCTGTCCAAAGCGGGGCGCTGTGAGGACCTTTGAGTCCATCCAGATGATGA 420  
QY 999 CCGTCTCTTACCGCTCTTCCAGAGGCGAGAAATGAATCCCTGATGAGTC 1058  
Db 421 CCGTCTCTTACCGCTCTTCCAGAGGCGAGAAATGAATCCCTGATGAGTC 480  
QY 1059 GGCCCTGTCATCTTCACTTTGAAGCAGATAATGACCGCATTAAGAGCGCTGACATC 1118  
Db 481 GGCCCTGTCATCTTCACTTTGAAGCAGATAATGACCGCATTAAGAGCGCTGACATC 540  
QY 1119 TTGTTACCGGAGCGAGGACAGCTGACCTGCGCTGCTCAAGTGAAGACATCCCTCG 1178  
Db 541 TTGTTACCGGAGCGAGGACAGCTGACCTGCGCTGCTCAAGTGAAGACATCCCTCG 600  
QY 1179 CAGCAGTGCCTCTTAACCATTTGACATCTTGTGAGCTGACATGATGCTCCCT 1238  
Db 601 CAGCAGTGCCTCTTAACCATTTGACATCTTGTGAGCTGACATGATGCTCCCT 660  
QY 1239 GGGAGTGTCCGACATGTGTGCGTGAATTCCTGCTTCAAGAGACAGGACCGCATGAC 1298  
Db 661 GGGAGTGTCCGACATGTGTGCGTGAATTCCTGCTTCAAGAGACAGGACCGCATGAC 720  
QY 1299 GTCTGTATGSCATATGCTTCAAGAACCACTCTGCTTGTGAGGACCAAAAGTGG 1358  
Db 721 GTCTGTATGSCATATGCTTCAAGAACCACTCTGCTTGTGAGGACCAAAAGTGG 780  
QY 1359 CAAGCTGAAGAG 1371  
Db 781 CAAGCTGAAGAG 793

RESULT 15  
US-10-245-739-91  
; Sequence 91, Application US/10245739  
; Publication No. US20030073195A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin  
APPLICANT: Bacon, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Marabhe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C96  
CURRENT FILING DATE: 2002-09-16  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 1997-09-17  
PRIOR FILING DATE: 1997-10-24  
PRIOR FILING DATE: 1997-10-24  
PRIOR FILING DATE: 1997-11-10  
PRIOR FILING DATE: 1998-03-27  
PRIOR FILING DATE: 1998-03-27  
PRIOR FILING DATE: 1998-05-22  
PRIOR FILING DATE: 1998-06-02  
PRIOR FILING DATE: 1998-06-18  
PRIOR FILING DATE: 1998-06-18  
PRIOR FILING DATE: 1998-06-24  
PRIOR FILING DATE: 1998-06-25  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-739-91

Query Match 13.9%; Score 793; DB 14; Length 2597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCGACCATCTTCCAGCCGGAACCTGACCAAGAACTTGAGGCGGATGGCAT 638  
DB 1 CGAGTATTTTCCGACCATCTTCCAGCCGGAACCTGACCAAGAACTTGAGGCGGATGGCAT 60  
QY 639 GTTGGCGTACGCTCTTCCATGATGAGTTCGTGCGCTCGATGATTAGATCCCTTCGACAC 698  
DB 61 GTTGGCGTACGCTCTTCCATGATGAGTTCGTGCGCTCGATGATTAGATCCCTTCGACAC 120  
QY 699 CTTACCATCATCCCTGATCTTGTATCTATGCTATGCTTATGAGTGGCACTT 758  
DB 121 CTTACCATCATCCCTGATCTTGTATCTATGCTATGCTTATGAGTGGCACTT 180  
QY 759 TGTCTACTTTTGAACCTTCCAGCTGAGATGATGCTTCCACAGGCTCCACACCAAGGA 818  
DB 181 TGTCTACTTTTGAACCTTCCAGCTGAGATGATGCTTCCACAGGCTCCACACCAAGGA 240  
QY 819 GCAAGTGATACATCCAGAGCTCGTGAAGCTTTGCAAGAGAGACACAGCCTTCAACTCCTA 878  
DB 241 GCAAGTGATACATCCAGAGCTCGTGAAGCTTTGCAAGAGAGACACAGCCTTCAACTCCTA 300  
QY 879 TGTAGAGGTGCCATGTGGCTGTGAGCGCAGTGGGTTGAGTACCGGCTGCTGAGGCTGC 938  
DB 301 TGTAGAGGTGCCATGTGGCTGTGAGCGCAGTGGGTTGAGTACCGGCTGCTGAGGCTGC 360

QY 939 CTACCTGTCCAAAGCCGGGGCGGTGCTTGGCAAGACCTTGGAGTTCATCCAGATGATGA 998  
DB 361 CTACCTGTCCAAAGCCGGGGCGGTGCTTGGCAAGACCTTGGAGTTCATCCAGATGATGA 420  
QY 999 CTTGCTTTCACCGCTTCTTCCAGAGGCGCAAGGCAAAATGAATCCCTGATGATGC 1058  
DB 421 CTTGCTTTCACCGCTTCTTCCAGAGGCGCAAGGCAAAATGAATCCCTGATGATGC 480  
QY 1059 GGGCTGTGATCTTATCTTGAAGCAATTAATGACCGCATTAAGAGAGGCTGCAATC 1118  
DB 481 GGGCTGTGATCTTATCTTGAAGCAATTAATGACCGCATTAAGAGAGGCTGCAATC 540  
QY 1119 TTGTTACCGGGGCGAGGCGACGCTGAGCTGAGCTCAAGGTGAAGGACATCCCTG 1178  
DB 541 TTGTTACCGGGGCGAGGCGACGCTGAGCTGAGCTCAAGGTGAAGGACATCCCTG 600  
QY 1179 CAGCAGTGGCTCTTAAACATTAAGCATTAATCTTGTGGCTTGAATGATCCCT 1238  
DB 601 CAGCAGTGGCTCTTAAACATTAAGCATTAATCTTGTGGCTTGAATGATCCCT 660  
QY 1239 GGGAGTGTCCGACATGATGCTGAGTTCCTGCTTCCAGAGGACAGGACCGCATGAC 1298  
DB 661 GGGAGTGTCCGACATGATGCTGAGTTCCTGCTTCCAGAGGACAGGACCGCATGAC 720  
QY 1299 GTCTGTATGCAATATGCTTAAAGAACCACTCTTGGCTTGTGGGACCAAAAGTG 1358  
DB 721 GTCTGTATGCAATATGCTTAAAGAACCACTCTTGGCTTGTGGGACCAAAAGTG 780  
QY 1359 CAAGCTGAAGAG 1371  
DB 781 CAAGCTGAAGAG 793

Search completed: February 20, 2004, 13:09:11  
Job time: 1311 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 02:24:55 : Search time 8736 Seconds  
(without alignments)  
19453.488 Million cell updates/sec

Title: US-09-964-956-12  
Perfect score: 5691  
Sequence: 1 atgaagaccatgcctcgtaa.....gcttagacacgtgaataaa 5691

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

EST:  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	637	11.2	838	14	CD653539 AGENCOURT
2	613	10.8	838	13	BK470595 DKF2P686G
3	457	8.0	483	9	AL707761 DKF2P686H
4	422	7.4	473	13	BK645676 DKF2P781K

5	328	5.8	564	10	BF953019
6	313	5.5	512	10	BF952116
7	232	4.1	232	9	AA077700
8	215	3.8	233	9	AA077556
9	206	3.6	251	9	AA077578
10	198	3.5	493	10	BF953008
11	176	3.1	924	10	BF312056
12	156	2.7	242	10	BF750764
13	152	2.7	789	12	BG216679
14	123	2.2	328	14	T07763
15	118	2.1	302	9	AA076688
16	115	2.0	317	10	BF750764
17	104	1.8	578	29	BSA408793
18	85	1.5	225	28	AQ356025
19	84	1.5	567	12	BM105323
20	84	1.5	690	12	BG718805
21	79	1.4	246	9	AA076683
22	73	1.3	273	9	AA076904
23	72	1.3	439	28	AA004244
24	71	1.2	285	28	AQ423495
25	62	1.1	420	28	AQ032236
26	54	1.0	390	28	AQ522248
27	54	0.9	745	14	CA316867
28	53	0.9	745	14	AK051614
29	53	0.9	3361	11	AK051614
30	49	0.9	712	12	BG424126
31	49	0.9	715	9	AU131481
32	49	0.9	862	13	BQ962177
33	49	0.9	5520	29	AY420666
34	47	0.8	202	10	BF759752
35	47	0.8	455	10	BF952937
36	47	0.8	498	14	CB130771
37	47	0.8	762	9	AL134739
38	47	0.8	865	14	CD243613
39	47	0.8	1027	12	BME44169
40	47	0.8	5341	29	AY420220
41	47	0.8	5691	29	AY420219
42	44	0.8	638	12	BG086250
43	43	0.8	720	12	BG820285
44	41	0.7	598	13	BK672058
45	41	0.7	657	13	BK670344
46	40	0.7	456	12	BM484361
47	39	0.7	439	10	BF801888
48	39	0.7	498	14	CB156432
49	39	0.7	536	10	BE296119
50	39	0.7	586	10	BE298119
51	39	0.7	628	14	CA868163
52	39	0.7	635	13	BQ447116
53	39	0.7	653	10	BE294546
54	39	0.7	688	12	BG21281
55	39	0.7	702	12	BG825770
56	39	0.7	710	10	BE295416
57	39	0.7	715	10	BE296475
58	39	0.7	732	10	BE296988
59	39	0.7	838	12	BI824913
60	39	0.7	882	13	BU149880
61	39	0.7	904	13	BQ720660
62	39	0.7	918	13	BQ723197
63	39	0.7	951	10	BF309302
64	39	0.7	994	10	BE736103
65	39	0.7	1059	12	BM547417
66	39	0.7	1201	9	AL529477
67	39	0.7	1445	10	BF734669
68	39	0.7	3520	29	AY420667
69	39	0.7	523	13	C84359
70	38	0.7	526	10	BF189217
71	38	0.7	587	14	CB521946
72	38	0.7	612	14	CA752450
73	38	0.7	677	14	CD351086
74	38	0.7	724	14	CA752378
75	38	0.7	733	14	CD351785
76	38	0.7	774	28	BZ192957
77	38	0.7	863	13	BU457242

BF953019	QV3-NN019
BF952116	QV1-NN022
AA077700	7B44B08 C
AA077556	7B19F10 C
AA077578	7B19H10 C
BF953008	QV3-NN019
BF312056	601897930
BF750764	7B18G11 C
BG216679	RST36373
T07763	EST05653 Fe
AA076688	7B03G05 C
BF750764	RC0-BN041
AJ408793	Homo sapi
AQ356025	CITB1-EL-
BM105323	508753 MA
BG718805	602695967
AA076691	7B04G03 C
AA076683	7B04F01 C
AA076904	7B04H08 C
AA004244	CIT-ESP-2
AQ423495	CITB1-EL-
AQ032236	HS_5200_A
AQ522248	UT-M-FW0-
CA316867	Mus muscu
AK051614	602448004
BG424126	602448004
AU131481	AU131481
BQ962177	AGENCOURT
AY420666	Homo sapi
BF759752	QV3-CT063
BF952937	QV3-NN019
CB130771	K-EST0180
AL134739	DKF2P547C
CD243613	AGENCOURT
BME44169	AGENCOURT
AY420220	Pan trogl
AY420219	Homo sapi
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BK672058	BK672058
BK670344	BK670344
BM484361	538194 MA
BP801888	CNO-C1009
CB156432	K-EST0215
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BE294546	601173485
BE296475	601174742
BE296988	601186342
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BQ723197	AGENCOURT
BF309302	601887769
BE736103	601305855
BM547417	AL529477
BF734669	601570457
AY420667	Pan trogl
C84359	C84359 oste
BF189217	234589 MA
CB521946	UI-M-GH0-
CA752450	UI-M-F00-
CD351086	UI-M-G10-
CA752378	UI-M-F00-
CD351785	UI-M-G10-
BZ192957	CH230-279
BU457242	603215856

78	38	0.7	5564	29	AY420221	Mus muscu
79	37	0.7	627	10	BA452530	BA452530
80	37	0.7	954	10	BU204192	BU204192
81	37	0.7	957	10	BF308474	BF308474
82	37	0.7	976	11	BU250116	BU250116
83	37	0.7	1428	11	AK051217	Mus muscu
84	36	0.6	830	29	CC906011	CC906011
85	35	0.6	412	12	BG694413	BG694413
86	35	0.6	523	13	BU349745	BU349745
87	35	0.6	594	14	CA361072	CA361072
88	35	0.6	623	13	BU347263	BU347263
89	35	0.6	678	13	BU269505	BU269505
90	35	0.6	678	13	BU269505	BU269505
91	35	0.6	684	13	BU268587	BU268587
92	35	0.6	684	13	BU268587	BU268587
93	35	0.6	715	13	BU282518	BU282518
94	35	0.6	721	13	BU368714	BU368714
95	35	0.6	745	13	BU394806	BU394806
96	35	0.6	752	13	BU262405	BU262405
97	35	0.6	759	13	BU262405	BU262405
98	35	0.6	782	13	BU268254	BU268254
99	35	0.6	787	13	BU251500	BU251500
100	35	0.6	794	13	BU251712	BU251712
101	35	0.6	798	13	BU318649	BU318649
102	35	0.6	844	13	BU371019	BU371019
103	34	0.6	453	14	CB546359	CB546359
104	34	0.6	513	14	CD555792	CD555792
105	34	0.6	555	14	CD555792	CD555792
106	34	0.6	600	13	BU321665	BU321665
107	34	0.6	637	28	BZ188915	BZ188915
108	34	0.6	872	12	BI150919	BI150919
109	34	0.6	911	12	BI905192	BI905192
110	34	0.6	3355	11	AK049319	AK049319
111	34	0.6	5447	29	AY420668	AY420668
112	33	0.6	208	14	CD547550	CD547550
113	33	0.6	243	10	AM894413	AM894413
114	33	0.6	287	14	CF535451	CF535451
115	33	0.6	291	14	CF727533	CF727533
116	33	0.6	339	14	CF727533	CF727533
117	33	0.6	359	13	BY210817	BY210817
118	33	0.6	410	13	BY226981	BY226981
119	33	0.6	426	14	CD552906	CD552906
120	33	0.6	502	14	CD355157	CD355157
121	33	0.6	502	14	CD803278	CD803278
122	33	0.6	595	13	BU611967	BU611967
123	33	0.6	600	14	CD351187	CD351187
124	33	0.6	648	14	CB248898	CB248898
125	33	0.6	664	14	CB290140	CB290140
126	33	0.6	667	14	CB249736	CB249736
127	33	0.6	678	13	BO180386	BO180386
128	33	0.6	687	14	CF746503	CF746503
129	33	0.6	699	14	CB527984	CB527984
130	33	0.6	704	13	BU249662	BU249662
131	33	0.6	713	14	CB249661	CB249661
132	33	0.6	714	14	CF534349	CF534349
133	33	0.6	715	14	CB722988	CB722988
134	33	0.6	727	14	CB247739	CB247739
135	33	0.6	727	14	CB247739	CB247739
136	33	0.6	751	13	BO444249	BO444249
137	33	0.6	751	13	CA374265	CA374265
138	33	0.6	782	14	CF743265	CF743265
139	33	0.6	798	14	CA752328	CA752328
140	33	0.6	805	14	CB246331	CB246331
141	33	0.6	821	14	CD802734	CD802734
142	33	0.6	823	14	CF537425	CF537425
143	33	0.6	829	14	CB722957	CB722957
144	33	0.6	831	14	CD349170	CD349170
145	33	0.6	862	14	CB724079	CB724079
146	33	0.6	862	14	CA511754	CA511754
147	32	0.6	422	14	CA886317	CA886317
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149	32	0.6	456	14	CB740636	AMGNMUC:M
150	32	0.6	533	10	BF076283	BF076283
151	32	0.6	537	9	AV604446	AV604446
152	32	0.6	554	14	CA887508	CA887508
153	32	0.6	565	9	AV591338	AV591338
154	32	0.6	612	10	BB656076	BB656076
155	32	0.6	632	14	CD352102	CD352102
156	32	0.6	753	12	BI786613	BI786613
157	32	0.6	774	12	BQ042277	BQ042277
158	32	0.6	809	13	BU610769	BU610769
159	32	0.6	833	14	CA321502	CA321502
160	32	0.6	906	13	BU841281	BU841281
161	32	0.6	2779	11	BC026974	BC026974
162	31	0.5	558	12	BM465817	BM465817
163	31	0.5	759	14	CA324071	CA324071
164	30	0.5	245	29	CE607027	CE607027
165	30	0.5	436	13	BY208069	BY208069
166	30	0.5	566	13	BU438837	BU438837
167	30	0.5	630	13	BU349288	BU349288
168	30	0.5	723	13	BU320195	BU320195
169	30	0.5	878	29	CNS0288E	CNS0288E
170	30	0.5	932	13	BU212882	BU212882
171	29	0.5	133	10	AW751258	AW751258
172	29	0.5	215	10	AW477697	AW477697
173	29	0.5	329	13	BO563192	BO563192
174	29	0.5	351	10	BF388606	BF388606
175	29	0.5	358	13	BY206562	BY206562
176	29	0.5	390	10	BF081206	BF081206
177	29	0.5	393	14	CB548039	CB548039
178	29	0.5	413	14	CF905124	CF905124
179	29	0.5	420	14	H63923	H63923
180	29	0.5	446	9	A1751311	A1751311
181	29	0.5	476	12	BM835173	BM835173
182	29	0.5	481	10	BF605400	BF605400
183	29	0.5	485	28	AO522271	AO522271
184	29	0.5	490	10	AM345695	AM345695
185	29	0.5	491	14	W19130	W19130
186	29	0.5	528	10	BE756300	BE756300
187	29	0.5	543	10	BE756306	BE756306
188	29	0.5	547	14	CD555307	CD555307
189	29	0.5	548	9	AM018699	AM018699
190	29	0.5	564	12	BI681117	BI681117
191	29	0.5	569	14	CA876752	CA876752
192	29	0.5	581	12	BI681252	BI681252
193	29	0.5	585	13	BU326136	BU326136
194	29	0.5	591	10	AM936163	AM936163
195	29	0.5	621	14	CD350875	CD350875
196	29	0.5	625	10	AM605180	AM605180
197	29	0.5	643	12	BG912949	BG912949
198	29	0.5	660	12	BM011540	BM011540
199	29	0.5	662	13	BO180468	BO180468
200	29	0.5	664	13	BO180472	BO180472
201	29	0.5	683	13	BU701512	BU701512
202	29	0.5	700	14	CB520195	CB520195
203	29	0.5	707	10	BE294007	BE294007
204	29	0.5	716	14	CA450292	CA450292
205	29	0.5	726	12	BI918365	BI918365
206	29	0.5	739	12	CB520485	CB520485
207	29	0.5	740	14	CA328914	CA328914
208	29	0.5	748	10	BF311719	BF311719
209	29	0.5	760	14	CF533779	CF533779
210	29	0.5	768	9	AU119341	AU119341
211	29	0.5	777	10	BE910224	BE910224
212	29	0.5	795	12	BI918234	BI918234
213	29	0.5	822	12	CD802878	CD802878
214	29	0.5	844	13	BO434703	BO434703
215	29	0.5	847	12	EG824951	EG824951
216	29	0.5	851	13	BQ878090	BQ878090
217	29	0.5	869	14	CD514755	CD514755
218	29	0.5	872	12	BI093605	BI093605
219	29	0.5	879	29	CNS023FH	CNS023FH
220	29	0.5	881	13	BO680140	BO680140
221	29	0.5	894	13	CA488958	CA488958
222	29	0.5	899	9	A1549788	A1549788
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224	0.5	899	13	B038111	AGENCOURT	297	25	0.4	659	13	B0394478
225	0.5	920	13	B0684665	AGENCOURT	298	25	0.4	687	13	B0290258
226	0.5	927	13	B0687297	AGENCOURT	299	25	0.4	693	13	B0236936
227	0.5	933	13	B0683335	AGENCOURT	300	25	0.4	711	14	B0519051
228	0.5	934	12	B0008857	603618623	301	25	0.4	716	14	B0249549
229	0.5	937	12	B0150733	AGENCOURT	302	25	0.4	725	12	B0950962
230	0.5	949	13	B0678617	AGENCOURT	303	25	0.4	732	14	CD803584
231	0.5	961	13	BQ708128	AGENCOURT	304	25	0.4	781	13	B0380892
232	0.5	972	10	BF304376	601887286	305	25	0.4	995	29	CNS03852
233	0.5	1102	10	BF310972	601887286	306	25	0.4	1142	28	CC321172
234	0.5	1201	9	AL544309	AL544309	307	24	0.4	269	14	CP176406
235	0.5	1562	10	BR402709	UT-R-CAO-	308	24	0.4	440	14	CP544396
236	0.5	658	28	A2710589	RCPI-24-1	309	24	0.4	591	14	CP554615
237	0.5	667	28	A2760778	IM0554D13	310	24	0.4	1006	29	CNS03XRL
238	0.5	707	13	B0682954	UT-CF-ECL	311	24	0.4	159	28	AQ006035
239	0.5	1037	13	B0117252	603139486	312	23	0.4	159	10	AM606478
240	0.5	1201	9	AL563454	AL563454	313	23	0.4	213	10	BE839128
241	0.5	431	28	BH301849	CH230-200	314	23	0.4	214	12	B1028112
242	0.5	436	14	BR4291486	AMGNNUC:M	315	23	0.4	214	29	CE077401
243	0.5	483	10	BR442398	259093 MA	316	23	0.4	222	14	CP567772
244	0.5	555	14	CA327930	UT-M-FYO-	317	23	0.4	256	14	CP520916
245	0.5	568	14	CB119832	UT-M-GHO-	318	23	0.4	264	14	CP177775
246	0.5	598	10	BE294865	601174145	319	23	0.4	277	10	BB330669
247	0.5	628	14	CB246297	UT-M-FYO-	320	23	0.4	320	9	AV591337
248	0.5	629	10	BB616077	BB616077	321	23	0.4	324	9	AT847593
249	0.5	649	29	AG173807	Pan crog1	322	23	0.4	336	10	BF404876
250	0.5	666	14	CF747010	UT-M-HBO-	323	23	0.4	342	10	BF375465
251	0.5	685	14	CP532783	UT-M-GHO-	324	23	0.4	350	13	BY010192
252	0.5	714	14	CF747064	UT-M-HBO-	325	23	0.4	364	10	BE711922
253	0.5	753	14	CF727396	UT-M-HBO-	326	23	0.4	366	10	BF396839
254	0.5	759	29	EX232664	Danio rer	327	23	0.4	420	9	A0233302
255	0.5	766	29	EX156364	Danio rer	328	23	0.4	421	13	B0362963
256	0.5	770	14	CB246327	UT-M-FYO-	329	23	0.4	438	10	BE955337
257	0.5	779	14	CB272736	UT-M-GHO-	330	23	0.4	444	28	AM462945
258	0.5	817	14	CB525253	UT-M-FYO-	331	23	0.4	454	10	AO928604
259	0.5	203	13	BUT01711	UT-M-FYO-	332	23	0.4	456	14	CB740772
260	0.5	244	14	R08384	YF19C03.R1	333	23	0.4	482	10	AM505130
261	0.5	402	14	AM024079	W062B11.X	334	23	0.4	504	10	BF404832
262	0.5	418	10	AM636330	B145D11.W	335	23	0.4	507	10	BF401338
263	0.5	426	28	AQ545955	CITBI-EI-	336	23	0.4	510	10	BF417952
264	0.5	429	10	AM487506	85041 MAR	337	23	0.4	524	12	B1343574
265	0.5	442	12	BG834999	353406 MA	338	23	0.4	531	9	AV615139
266	0.5	523	9	AA629363	ZU78A05.S	339	23	0.4	537	12	BG988314
267	0.5	529	12	B1847501	469353 MA	340	23	0.4	538	10	BE664819
268	0.5	552	9	AL798589	AL798589	341	23	0.4	538	14	CB432783
269	0.5	572	9	AU169163	AU169163	342	23	0.4	558	9	AT353444
270	0.5	624	12	BM312244	1941807.Y	343	23	0.4	571	10	BE965210
271	0.5	642	9	AL781854	AL781854	344	23	0.4	593	14	CA381535
272	0.5	655	9	AL710127	DKE2P686A	345	23	0.4	594	29	CE724299
273	0.5	666	14	CF747312	UT-M-HBO-	346	23	0.4	610	14	CA379844
274	0.5	695	9	AL710133	DKE2P686B	347	23	0.4	620	10	CD497380
275	0.5	699	9	AL710220	DKE2P686P	348	23	0.4	635	14	CB519047
276	0.5	706	13	EX781817	EX781817	349	23	0.4	650	9	AL595528
277	0.5	724	14	CF286881	AGENCOURT	350	23	0.4	665	13	B0432459
278	0.5	729	13	BQ696918	QHB39015.	351	23	0.4	676	14	BE950572
279	0.5	770	13	EX781815	EX781815	352	23	0.4	676	14	CD348043
280	0.5	774	13	EX781811	EX781811	353	23	0.4	703	14	CA354740
281	0.5	785	29	CNS03DV2	AL2339591	354	23	0.4	716	10	AM128424
282	0.5	867	13	EX723674	Tetracodon	355	23	0.4	716	12	BM671652
283	0.5	871	29	CNS032PS	AL225145	356	23	0.4	716	13	B0574441
284	0.5	906	13	B1364545	603786848	357	23	0.4	735	14	CF737273
285	0.5	959	29	CNS04LOZ	AL2296356	358	23	0.4	737	14	CA512978
286	0.5	965	29	CNS020V4	Tetracodon	359	23	0.4	751	12	E1524948
287	0.5	967	10	BE902192	601675217	360	23	0.4	789	13	EX320194
288	0.5	996	9	AA348083	EST54487	361	23	0.4	789	12	B1161615
289	0.5	1000	10	BE806831	QV1-BT067	362	23	0.4	860	29	CNS02CHV
290	0.5	433	10	BE721791	189611 MA	363	23	0.4	884	10	BE737260
291	0.5	460	10	BE809818	215687 MA	364	23	0.4	901	13	BQ959274
292	0.5	504	14	CA542722	C0623B05-	365	23	0.4	906	13	B0947921
293	0.5	589	13	BQ395092	NISC.Mg13	366	23	0.4	929	13	B0916279
294	0.5	606	14	CA387176	668992 NC	367	23	0.4	951	13	BQ920360
295	0.5	612	13	B0290154	604162679	368	23	0.4	999	13	B0073659
296	0.5	657	9	AL710145	DKE2P686D	369	23	0.4	1008	12	BM553544

370	23	0.4	1147	12	EM474534	ACENCOURT	C 443	21	0.4	613	14	CF072243	CF072243	FEL 2 HQ7
371	23	0.4	6885	11	AF54895	Xenopus I	444	21	0.4	629	10	BB656644	BB656644	BB656644
372	22	0.4	196	9	AA146257	mq46c12.r	445	21	0.4	634	13	BY737421	BY737421	BY737421
373	22	0.4	197	12	BI794488	IC90907.y	446	21	0.4	635	28	BH295836	BH295836	BH295836
374	22	0.4	219	13	BQ306474	MRO-BT300	C 447	21	0.4	639	12	BM939457	BM939457	BM939457
375	22	0.4	242	9	AA655055	vv12f07.r	C 448	21	0.4	643	12	BM933777	BM933777	BM933777
376	22	0.4	321	13	BY346505	BY346505	449	21	0.4	645	14	BU702897	BU702897	BU702897
377	22	0.4	333	13	BY346505	BY346505	450	21	0.4	645	14	CF904478	CF904478	CF904478
378	22	0.4	397	10	BE372210	BE372210	C 451	21	0.4	661	14	CP424271	CP424271	CP424271
379	22	0.4	400	13	BY310735	BY310735	C 452	21	0.4	661	14	CF732133	CF732133	CF732133
380	22	0.4	412	28	AAQ973881	RPCI-23-3	C 453	21	0.4	667	10	BB653300	BB653300	BB653300
381	22	0.4	445	13	BY630457	BY630457	C 454	21	0.4	704	12	BI134654	BI134654	BI134654
382	22	0.4	442	9	AA144090	mq62h03.r	C 455	21	0.4	708	12	BI658106	BI658106	BI658106
383	22	0.4	458	12	BF774252	283849.y	456	21	0.4	715	28	BH973878	BH973878	BH973878
384	22	0.4	488	12	BI499454	IC58409.y	457	21	0.4	707	13	BY763622	BY763622	BY763622
385	22	0.4	538	10	BB763000	BB763000	C 458	21	0.4	720	14	CD231662	CD231662	CD231662
386	22	0.4	570	28	AZ994244	2M0279PF8	C 459	21	0.4	731	14	CB953986	CB953986	CB953986
387	22	0.4	594	12	EG087906	HS146C10-	C 460	21	0.4	732	13	BU610785	BU610785	BU610785
388	22	0.4	595	13	BU445924	603764774	C 461	21	0.4	732	13	CA056714	CA056714	CA056714
389	22	0.4	600	12	BI988602	4013-18 M	C 462	21	0.4	732	14	CD804196	CD804196	CD804196
390	22	0.4	602	13	BQ308092	MRO-BT300	C 463	21	0.4	746	10	BF669458	BF669458	BF669458
391	22	0.4	616	13	BU002750	OCG33002.	C 464	21	0.4	749	14	CF539032	CF539032	CF539032
392	22	0.4	633	13	BB651957	BB651957	C 465	21	0.4	751	12	BM946881	BM946881	BM946881
393	22	0.4	656	13	BY720942	BY720942	C 466	21	0.4	753	13	BU646958	BU646958	BU646958
394	22	0.4	658	10	BB079093	BB079093	C 467	21	0.4	753	14	CF870392	CF870392	CF870392
395	22	0.4	672	12	BU068041	BU068041	C 468	21	0.4	753	12	AG184652	AG184652	AG184652
396	22	0.4	672	12	BM489469	Pgm21.pko	C 469	21	0.4	774	12	BI854656	BI854656	BI854656
397	22	0.4	707	14	CF950494	UI-M-HLO-	C 470	21	0.4	774	13	BQ572343	BQ572343	BQ572343
398	22	0.4	741	14	CF735159	UI-M-HBO-	C 471	21	0.4	780	9	AU080551	AU080551	AU080551
399	22	0.4	871	10	BF204222	601867675	C 472	21	0.4	786	9	AI173889	AI173889	AI173889
400	22	0.4	907	14	CB204955	AGENCOURT	C 473	21	0.4	803	10	BE512932	BE512932	BE512932
401	22	0.4	910	14	CF583738	CF583738	C 474	21	0.4	803	28	BH393050	BH393050	BH393050
402	22	0.4	931	10	BE858586	BE858586	C 475	21	0.4	805	13	BU709473	BU709473	BU709473
403	22	0.4	971	13	BY718234	BY718234	C 476	21	0.4	806	14	CB900573	CB900573	CB900573
404	22	0.4	990	13	BQ918649	AGENCOURT	C 477	21	0.4	809	29	CNS0303G	CNS0303G	CNS0303G
405	22	0.4	1174	12	BM479213	BM479213	C 478	21	0.4	817	13	BU614197	BU614197	BU614197
406	22	0.4	1570	11	AK034100	Mus muscu	C 479	21	0.4	819	14	CD353586	CD353586	CD353586
407	22	0.4	1814	11	AK018097	AK018097	C 480	21	0.4	820	14	CA450715	CA450715	CA450715
408	21	0.4	267	28	CC556494	PURFER07B	C 481	21	0.4	829	14	CF730532	CF730532	CF730532
409	21	0.4	292	12	BI342056	BI342056	C 482	21	0.4	831	12	BI735472	BI735472	BI735472
410	21	0.4	301	9	AA077378	7B14D10.C	C 483	21	0.4	834	12	CA315530	CA315530	CA315530
411	21	0.4	323	13	BY128741	BY128741	C 484	21	0.4	834	14	CNS0422W	CNS0422W	CNS0422W
412	21	0.4	345	10	AM347841	AM347841	C 485	21	0.4	852	13	BQ929727	BQ929727	BQ929727
413	21	0.4	347	14	CB546028	AMGNNUC.N	C 486	21	0.4	863	13	BQ922139	BQ922139	BQ922139
414	21	0.4	348	14	F11945	HSC33F101.n	C 487	21	0.4	877	14	CA476162	CA476162	CA476162
415	21	0.4	399	13	BQ349459	MR2-HT037	C 488	21	0.4	887	13	BU855411	BU855411	BU855411
416	21	0.4	403	14	CB768239	AMGNNUC.S	C 489	21	0.4	894	14	CR182577	CR182577	CR182577
417	21	0.4	412	13	BY533492	BY533492	C 490	21	0.4	935	12	BG423548	BG423548	BG423548
418	21	0.4	415	10	AM898023	AM898023	C 491	21	0.4	947	29	CNS038BV	CNS038BV	CNS038BV
419	21	0.4	431	14	CB800131	AMGNNUC.N	C 492	21	0.4	960	13	CA476779	CA476779	CA476779
420	21	0.4	436	28	BI137551	CH230-256	C 493	21	0.4	971	13	BQ945270	BQ945270	BQ945270
421	21	0.4	440	13	BY536419	BY536419	C 494	21	0.4	971	13	BQ888076	BQ888076	BQ888076
422	21	0.4	444	13	BY535502	BY535502	C 495	21	0.4	986	12	BG421069	BG421069	BG421069
423	21	0.4	453	10	AM488782	UI-M-BH3-	C 496	21	0.4	1038	29	CNS0423C	CNS0423C	CNS0423C
424	21	0.4	473	13	CF072986	CF072986	C 497	21	0.4	1065	12	BM543333	BM543333	BM543333
425	21	0.4	476	14	AM564124	IC1_282.F	C 500	21	0.4	1086	12	CNS058X1	CNS058X1	CNS058X1
426	21	0.4	485	10	BE650811	UI-M-BH3-	C 501	21	0.4	1094	29	AY403184	AY403184	AY403184
427	21	0.4	492	10	BE650811	UI-M-BH3-	C 502	21	0.4	1491	29	BF133668	BF133668	BF133668
428	21	0.4	511	28	BZ247757	EM1_15.HO	C 503	21	0.4	1589	10	AA187559	AA187559	AA187559
429	21	0.4	513	12	BG322938	CC328180	C 504	21	0.4	2225	11	AK083185	AK083185	AK083185
430	21	0.4	513	28	CC328180	OGU447TH	C 505	21	0.4	2676	11	AK083476	AK083476	AK083476
431	21	0.4	519	14	CB681756	OSJNBF08G	C 506	21	0.4	3043	11	AK051425	AK051425	AK051425
432	21	0.4	536	10	BE594409	601311366	C 507	21	0.4	105	9	AI940126	AI940126	AI940126
433	21	0.4	548	14	BE345195	BE345195	C 508	21	0.4	122	12	BG984330	BG984330	BG984330
434	21	0.4	553	28	AZ097801	RRC1-23-4	C 509	21	0.4	133	10	AM633072	AM633072	AM633072
435	21	0.4	562	10	AM658222	108357.MA	C 510	21	0.4	148	28	CA418759	CA418759	CA418759
436	21	0.4	564	29	CE598162	1igr-gs8-	C 511	21	0.4	150	9	AA299609	AA299609	AA299609
437	21	0.4	570	12	CF795370	891499.MA	C 512	21	0.4	151	9	AA186515	AA186515	AA186515
438	21	0.4	579	14	BI680360	458603.MA	C 513	21	0.4	152	10	AM606479	AM606479	AM606479
439	21	0.4	582	14	CB586806	AMGNNUC.N	C 514	21	0.4	158	14	NB5298	NB5298	NB5298
440	21	0.4	601	10	BE295227	601175212	C 515	21	0.4	158	14	NB5298	NB5298	NB5298
441	21	0.4	604	14	CA729320	Wd11c.pko	C 515	21	0.4	158	14	NB5298	NB5298	NB5298
442	21	0.4	604	14	CA729320	Wd11c.pko	C 515	21	0.4	158	14	NB5298	NB5298	NB5298

C 516	20	0.4	159	9	AA324238	EST72311	C 589	20	0.4	280	9	AA374932	AA374932	EST78742
C 517	20	0.4	165	9	AA054826	F1-1381D	C 590	20	0.4	281	13	BY363416	BY363416	EST363416
C 518	20	0.4	169	10	BF350837	MR2-HT037	C 591	20	0.4	282	9	AA327042	AA327042	EST30580
C 519	20	0.4	169	13	BQ349149	MR2-HT037	C 592	20	0.4	282	14	CK228377	CK228377	701940666
C 520	20	0.4	171	9	AA303515	EST16417	C 593	20	0.4	284	9	AA321842	AA321842	EST24407
C 521	20	0.4	176	14	R57940	F7782 Petal	C 594	20	0.4	284	9	AA373219	AA373219	EST85225
C 522	20	0.4	179	10	BF797284	602256902	C 595	20	0.4	287	10	AA407102	AA407102	UT-HF-BLO
C 523	20	0.4	181	10	BE062702	OYO-HT026	C 596	20	0.4	287	10	D55985	D55985	HUM409F02B
C 524	20	0.4	182	10	BF174924	MYE4061 M	C 597	20	0.4	288	10	BF758168	BF758168	CY4-CT057
C 525	20	0.4	183	14	CB115282	K-EST0160	C 598	20	0.4	288	9	AA327632	AA327632	EST311006
C 526	20	0.4	192	12	BE847370	K-EST0126	C 599	20	0.4	289	9	AA359623	AA359623	EST168755
C 527	20	0.4	199	10	BE272901	601111178	C 600	20	0.4	290	9	AA316107	AA316107	EST187830
C 528	20	0.4	205	14	D53311	HUM105805B	C 601	20	0.4	290	9	AA380757	AA380757	EST93771
C 529	20	0.4	207	9	AA354394	EST62865	C 602	20	0.4	291	9	AA369717	AA369717	EST81160
C 530	20	0.4	207	12	BM855358	K-EST0138	C 603	20	0.4	292	14	N85715	N85715	J4709F Huma
C 531	20	0.4	214	10	AM250280	2821291.5	C 604	20	0.4	294	9	AA303651	AA303651	EST16300
C 532	20	0.4	216	14	CP182546	UT-M-BYO-	C 605	20	0.4	294	9	AA360956	AA360956	EST70160
C 533	20	0.4	227	9	AA344981	EST51103	C 606	20	0.4	296	12	BM707658	BM707658	UT-F-CT1-
C 534	20	0.4	227	9	AA380618	EST93678	C 607	20	0.4	296	12	BM759123	BM759123	K-EST0039
C 535	20	0.4	228	9	AA378455	EST91152	C 608	20	0.4	299	9	AA319628	AA319628	EST21898
C 536	20	0.4	228	13	BQ316716	PMO-CT032	C 609	20	0.4	299	9	AA299524	AA299524	EST12044
C 537	20	0.4	229	9	AA348975	EST55515	C 610	20	0.4	300	9	AU098629	AU098629	EST98629
C 538	20	0.4	230	9	A1630538	ad12b03.Y	C 611	20	0.4	300	9	AA301672	AA301672	EST14707
C 539	20	0.4	232	10	BF176264	MYE6724 M	C 612	20	0.4	300	13	C15642	C15642	EST14707
C 540	20	0.4	232	13	B0084239	K-EST0148	C 613	20	0.4	301	14	N87533	N87533	LI1553F Huma
C 541	20	0.4	233	9	AA095629	15320.8eq	C 614	20	0.4	303	9	AA300193	AA300193	EST12823
C 542	20	0.4	233	14	CD693629	EST10152	C 615	20	0.4	306	14	CB114361	CB114361	EST30898
C 543	20	0.4	234	10	AA404893	UT-HF-BLO	C 616	20	0.4	306	14	N88339	N88339	K3125F Huma
C 544	20	0.4	234	10	BB848214	BB848214	C 617	20	0.4	306	14	N88339	N88339	K3125F Huma
C 545	20	0.4	234	14	N89467	LY1179F Huma	C 618	20	0.4	308	10	AA379387	AA379387	EST92250
C 546	20	0.4	235	9	AA317384	EST19319	C 619	20	0.4	308	10	AA408211	AA408211	UT-HF-BLO
C 547	20	0.4	235	10	AA378168	EST90924	C 620	20	0.4	308	14	CB107775	CB107775	K-EST0147
C 548	20	0.4	235	10	BF176302	MYE6776 M	C 621	20	0.4	309	13	BO084407	BO084407	EST34218
C 549	20	0.4	236	10	BE391698	601285918	C 622	20	0.4	310	9	AA774454	AA774454	EST34218
C 550	20	0.4	237	10	BE182717	KC3-HT065	C 623	20	0.4	310	9	AA303825	AA303825	EST16492
C 551	20	0.4	238	10	BE709025	QV2-HT057	C 624	20	0.4	311	14	T33057	T33057	EST16492
C 552	20	0.4	239	10	BE709073	QV2-HT057	C 625	20	0.4	311	14	BG944013	BG944013	ax45d03.x
C 553	20	0.4	239	9	AA379511	EST92358	C 626	20	0.4	312	14	N86184	N86184	KK844F Huma
C 554	20	0.4	241	14	CK228356	700932458	C 627	20	0.4	312	14	N86184	N86184	KK844F Huma
C 555	20	0.4	242	9	AA320506	EST22866	C 628	20	0.4	317	9	AA379584	AA379584	EST92485
C 556	20	0.4	242	12	BM845329	K-EST0123	C 629	20	0.4	317	14	N84395	N84395	YV65h10.t1
C 557	20	0.4	243	12	BM831254	K-EST0105	C 630	20	0.4	320	14	H84395	H84395	YV65h10.t1
C 558	20	0.4	244	13	B0084234	K-EST0148	C 631	20	0.4	323	9	AA362957	AA362957	EST72819
C 559	20	0.4	251	14	CB114327	K-EST0157	C 632	20	0.4	324	9	AA296674	AA296674	EST12216
C 560	20	0.4	251	14	W46597	zc32911.t1	C 633	20	0.4	324	9	AA436473	AA436473	ZV08e08.s
C 561	20	0.4	252	14	W21121	2b57a09.t1	C 634	20	0.4	329	12	BP432650	BP432650	EST99590
C 562	20	0.4	254	9	AA379264	EST92293	C 635	20	0.4	329	12	BP432650	BP432650	EST99590
C 563	20	0.4	255	10	BF841625	MR1-HT106	C 636	20	0.4	329	14	CD708234	CD708234	EST24761
C 564	20	0.4	255	14	CB117774	K-EST0163	C 637	20	0.4	330	9	AA332349	AA332349	EST36363
C 565	20	0.4	256	9	AA093478	KH8157.se	C 638	20	0.4	332	9	AA056711	AA056711	2166F06.F
C 566	20	0.4	256	9	AT940120	R01-CT003	C 639	20	0.4	332	9	AA378649	AA378649	EST92515
C 567	20	0.4	256	10	BF445924	7P16d077.x	C 640	20	0.4	333	10	BE378407	BE378407	60126738
C 568	20	0.4	258	9	AA334037	EST38186	C 641	20	0.4	335	9	AA378914	AA378914	EST91666
C 569	20	0.4	258	13	BQ302910	MR2-BT059	C 642	20	0.4	335	9	AA376559	AA376559	EST88893
C 570	20	0.4	259	9	AA089673	chm0403.s	C 643	20	0.4	340	9	AA316739	AA316739	EST188474
C 571	20	0.4	260	14	CK228374	701881964	C 644	20	0.4	340	9	AA354788	AA354788	EST63101
C 572	20	0.4	261	14	N83648	KX1702F Huma	C 645	20	0.4	340	12	BP430081	BP430081	EST63101
C 573	20	0.4	262	9	AA092328	116679.se	C 646	20	0.4	340	12	BP430081	BP430081	EST63101
C 574	20	0.4	262	9	AA370834	EST82584	C 647	20	0.4	340	14	CB143463	CB143463	in65h02.Y
C 575	20	0.4	264	10	AA384255	MR2-HT037	C 648	20	0.4	341	10	AY683689	AY683689	K-EST0197
C 576	20	0.4	266	9	AA374881	EST87250	C 649	20	0.4	341	10	AM405432	AM405432	UT-HF-BLO
C 577	20	0.4	267	9	AA374519	EST86558	C 650	20	0.4	343	12	BM745901	BM745901	K-EST0019
C 578	20	0.4	267	10	BF922403	QV2-NT014	C 651	20	0.4	343	14	T16854	T16854	N1B193-5R
C 579	20	0.4	267	12	BM746339	K-EST0020	C 652	20	0.4	344	14	CA780661	CA780661	ME1384.7-
C 580	20	0.4	268	9	AA355580	EST64086	C 653	20	0.4	345	9	AI094196	AI094196	ga29d07.b
C 581	20	0.4	272	9	AA300909	EST13862	C 654	20	0.4	345	13	BO462268	BO462268	EST69396
C 582	20	0.4	273	9	AA326337	n117b12.b	C 655	20	0.4	345	13	BO462268	BO462268	EST69396
C 583	20	0.4	274	9	AA396596	EST11147	C 656	20	0.4	345	13	CO2952	CO2952	CO2952
C 584	20	0.4	275	9	AA301191	EST14104	C 657	20	0.4	345	14	T31443	T31443	EST12585.Hu
C 585	20	0.4	275	9	AA301191	EST14104	C 658	20	0.4	346	9	AA317760	AA317760	EST19741
C 586	20	0.4	275	9	AA329861	EST33520	C 659	20	0.4	347	9	AA363102	AA363102	EST72928
C 587	20	0.4	277	9	AA337150	EST42112	C 660	20	0.4	348	12	BP430056	BP430056	EST72928
C 588	20	0.4	278	14	CB139463	K-EST0192	C 661	20	0.4	350	9	AA095160	AA095160	cp3028.se

C 662	20	0.4	350	9	AV657207	AV657207	AV657207	C 735	20	0.4	399	12	BM697932	BM697932	UI-E-DX0-
C 663	20	0.4	350	14	CA541538	CA541538	CA541538	C 736	20	0.4	399	12	BM765131	BM765131	K-EST0046
C 664	20	0.4	350	14	CB265451	CB265451	CB265451	C 737	20	0.4	400	13	BM316717	BM316717	PMO-CT032
C 665	20	0.4	353	12	BM698372	BM698372	UI-E-DX0-	C 738	20	0.4	402	9	AA315627	AA315627	EST187444
C 666	20	0.4	353	13	BU954892	BU954892	AGENCOURT	C 739	20	0.4	402	14	CB110435	CB110435	K-EST0151
C 667	20	0.4	355	9	AV660935	AV660935	AGENCOURT	C 740	20	0.4	403	13	BQ302024	BQ302024	PM3-BT033
C 668	20	0.4	355	9	AV687152	AV687152	AGENCOURT	C 741	20	0.4	403	14	CA348966	CA348966	1930109.Y
C 669	20	0.4	356	12	BM838841	BM838841	K-EST0115	C 742	20	0.4	403	14	W07028	W07028	2A31H06.r1
C 670	20	0.4	357	9	AA310685	AA310685	EST181499	C 743	20	0.4	404	9	AA315752	AA315752	2044908.r
C 671	20	0.4	358	9	AV689298	AV689298	AGENCOURT	C 744	20	0.4	404	9	AA35061	AA35061	EST175745
C 672	20	0.4	358	9	AA378175	AA378175	AGENCOURT	C 745	20	0.4	404	12	BM644227	BM644227	K-EST0122
C 673	20	0.4	358	13	BU589595	BU589595	AGENCOURT	C 746	20	0.4	404	13	BQ316399	BQ316399	PMO-CT032
C 674	20	0.4	360	9	AA092605	AA092605	AGENCOURT	C 747	20	0.4	404	13	BQ349172	BQ349172	MR2-HT037
C 675	20	0.4	361	9	AA334401	AA334401	EST38611	C 748	20	0.4	405	9	AA327191	AA327191	EST30495
C 676	20	0.4	362	12	BM784746	BM784746	K-EST0063	C 749	20	0.4	405	10	BE280351	BE280351	601158605
C 677	20	0.4	363	9	AA545754	AA545754	HMSFTC2-	C 750	20	0.4	405	13	BY650605	BY650605	BY650605
C 678	20	0.4	363	10	BF170190	BF170190	PCL0378 M	C 751	20	0.4	406	12	BG686511	BG686511	602637461
C 679	20	0.4	364	14	CA563301	CA563301	K0312C11-	C 752	20	0.4	406	12	BM634962	BM634962	K-EST0110
C 680	20	0.4	366	9	AA657772	AA657772	ni06E02.s	C 753	20	0.4	406	14	CB109990	CB109990	K-EST0151
C 681	20	0.4	366	9	AA083546	AA083546	zn39a12.r	C 754	20	0.4	406	14	CB114314	CB114314	K-EST0157
C 682	20	0.4	366	12	BI021550	BI021550	CM3-WT034	C 755	20	0.4	407	9	AV763747	AV763747	AV763747
C 683	20	0.4	366	13	BQ349182	BQ349182	MR2-HT037	C 756	20	0.4	407	9	AA506018	AA506018	ni02804.s
C 684	20	0.4	367	12	BM761700	BM761700	K-EST0042	C 757	20	0.4	407	12	BM636012	BM636012	K-EST0111
C 685	20	0.4	368	9	AA314463	AA314463	v201109.r	C 758	20	0.4	407	13	BQ349228	BQ349228	MR2-HT037
C 686	20	0.4	368	12	BI710858	BI710858	1d92H01.Y	C 759	20	0.4	408	10	AM406770	AM406770	UI-HF-BL0
C 687	20	0.4	369	9	AA380091	AA380091	EST93024	C 760	20	0.4	408	12	BM649673	BM649673	K-EST0129
C 688	20	0.4	370	10	AA456469	AA456469	UI-M-BH3-	C 761	20	0.4	408	12	BM744829	BM744829	K-EST0018
C 689	20	0.4	370	29	CE489047	CE489047	CI9T-G88-	C 762	20	0.4	409	13	BQ349008	BQ349008	MR2-HT037
C 690	20	0.4	374	12	BP431251	BP431251	BP431251	C 763	20	0.4	409	13	BM483998	BM483998	K-EST0068
C 691	20	0.4	375	9	AA1130268	AA1130268	SMC0V3CN	C 764	20	0.4	410	9	AA379891	AA379891	EST97783
C 692	20	0.4	375	12	BM716419	BM716419	UI-E-DX0-	C 765	20	0.4	410	9	BF975799	BF975799	602246363
C 693	20	0.4	377	14	W07669	W07669	zbd4e08.r1	C 766	20	0.4	411	10	BE276230	BE276230	601144312
C 694	20	0.4	377	14	W24570	W24570	zbd4e08.r1	C 767	20	0.4	411	12	BM687475	BM687475	UI-E-CR0-
C 695	20	0.4	378	12	BM754157	BM754157	K-EST0031	C 768	20	0.4	411	12	BM785068	BM785068	K-EST0063
C 696	20	0.4	378	14	CB107461	CB107461	K-EST0146	C 769	20	0.4	412	9	AA377959	AA377959	EST90602
C 697	20	0.4	379	9	AA157651	AA157651	2046E08.r	C 770	20	0.4	412	12	BM799435	BM799435	K-EST0083
C 698	20	0.4	379	9	AA305115	AA305115	EST176116	C 771	20	0.4	412	13	BQ084071	BQ084071	K-EST0147
C 699	20	0.4	379	12	BI134178	BI134178	UI-M-BH3-	C 772	20	0.4	413	13	BQ0849120	BQ0849120	MR2-HT037
C 700	20	0.4	382	12	BM766498	BM766498	K-EST0062	C 773	20	0.4	413	13	BM316032	BM316032	BM316032
C 701	20	0.4	382	12	BM798583	BM798583	K-EST0082	C 774	20	0.4	413	14	CA3770160	CA3770160	CA3770160
C 702	20	0.4	382	12	BM855116	BM855116	K-EST0137	C 775	20	0.4	414	9	AA384750	AA384750	EST96412
C 703	20	0.4	382	14	CD687892	CD687892	EST4413.h	C 776	20	0.4	414	13	BM316033	BM316033	BM316033
C 704	20	0.4	383	14	BF174356	BF174356	MYE3029 M	C 777	20	0.4	414	13	BM316265	BM316265	BM316265
C 705	20	0.4	384	10	BE127750	BE127750	DEPA1499	C 778	20	0.4	415	13	BY155714	BY155714	BY155714
C 706	20	0.4	384	12	BM857283	BM857283	K-EST0141	C 779	20	0.4	415	13	W24421	W24421	zbd6e011.r1
C 707	20	0.4	386	9	AA345769	AA345769	EST5024	C 780	20	0.4	415	14	W24421	W24421	zbd6e011.r1
C 708	20	0.4	387	9	AA933751	AA933751	CM59E02.s	C 781	20	0.4	416	10	AA580062	AA580062	MR2-HT037
C 709	20	0.4	387	10	BE741611	BE741611	601594930	C 782	20	0.4	416	12	BM676838	BM676838	MR2-HT037
C 710	20	0.4	388	9	AA770958	AA770958	VE14A.O.r	C 783	20	0.4	416	13	BQ349050	BQ349050	MR2-HT037
C 711	20	0.4	388	12	BM773102	BM773102	K-EST0057	C 784	20	0.4	416	14	CB121844	CB121844	K-EST0169
C 712	20	0.4	388	14	CA388851	CA388851	CS03D02.Y	C 785	20	0.4	417	12	BM646469	BM646469	K-EST0125
C 713	20	0.4	388	14	CA866681	CA866681	1r74h01.Y	C 786	20	0.4	417	13	BQ349026	BQ349026	MR2-HT037
C 714	20	0.4	388	14	W21418	W21418	zbd6b12.r1	C 787	20	0.4	418	10	BF350828	BF350828	MR2-HT037
C 715	20	0.4	390	10	AA663232	AA663232	h76608.Y	C 788	20	0.4	418	12	BG876940	BG876940	MR2-HT037
C 716	20	0.4	390	12	BM794655	BM794655	K-EST0062	C 789	20	0.4	418	13	BQ349044	BQ349044	MR2-HT037
C 717	20	0.4	390	12	BM794655	BM794655	K-EST0062	C 790	20	0.4	418	14	W05304	W05304	W05304
C 718	20	0.4	390	13	EQ333257	EQ333257	KCS-PT000	C 791	20	0.4	419	9	AV760412	AV760412	AV760412
C 719	20	0.4	391	13	EQ39028	EQ39028	MR2-HT037	C 792	20	0.4	419	12	BG876932	BG876932	MR2-HT037
C 720	20	0.4	391	13	BY618586	BY618586	BY618586	C 793	20	0.4	419	12	BM645957	BM645957	K-EST0124
C 721	20	0.4	393	10	BM900164	BM900164	HOA35-1-E	C 794	20	0.4	419	14	W19623	W19623	2b35D09.r1
C 722	20	0.4	393	13	BM316421	BM316421	MR2-HT037	C 795	20	0.4	420	10	BF922400	BF922400	QV2-NT014
C 723	20	0.4	394	13	BM316421	BM316421	MR2-HT037	C 796	20	0.4	420	10	BM645957	BM645957	K-EST0125
C 724	20	0.4	395	10	AA580130	AA580130	PMO-CT032	C 797	20	0.4	420	13	BQ349012	BQ349012	MR2-HT037
C 725	20	0.4	395	10	AA580130	AA580130	PMO-CT032	C 798	20	0.4	420	13	BQ349012	BQ349012	MR2-HT037
C 726	20	0.4	395	12	BM773095	BM773095	UI-E-CIT-	C 799	20	0.4	420	13	BQ349012	BQ349012	MR2-HT037
C 727	20	0.4	395	14	HI9560	HI9560	Ym4H04.r1	C 800	20	0.4	420	14	CB298274	CB298274	220009.r1
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C 729	20	0.4	396	12	BM760472	BM760472	K-EST0041	C 802	20	0.4	421	12	BG876935	BG876935	MR2-HT037
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C 731	20	0.4	397	9	AA304574	AA304574	EST17580	C 804	20	0.4	421	13	BQ349181	BQ349181	MR2-HT037
C 732	20	0.4	397	14	CA943150	CA943150	1p33C07.Y	C 805	20	0.4	423	9	AA310988	AA310988	EST181780
C 733	20	0.4	397	14	T81938	T81938	Yd04A11.r1	C 806	20	0.4	423	9	BR041547	BR041547	6053D07.x
C 734	20	0.4	398	9	AV708620	AV708620	AV708620	C 807	20	0.4	423	13	BQ316422	BQ316422	PMO-CT032

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809	20	0.4	423	13	BQ349014	MR2-HT037	882	20	0.4	448	14	CF156829	CF156829
810	20	0.4	423	13	BQ362859	PM1-ST026	883	20	0.4	448	14	W21304	W21304
811	20	0.4	424	9	AA002219	z85h01.x	884	20	0.4	449	9	AA881406	AA881406
812	20	0.4	424	13	BQ349043	MR2-HT037	885	20	0.4	449	9	AA082310	AA082310
813	20	0.4	424	13	BQ349128	MR2-HT037	886	20	0.4	449	9	AA212820	AA212820
814	20	0.4	424	13	BQ349148	MR2-HT037	887	20	0.4	449	13	BQ316420	BQ316420
815	20	0.4	424	14	CA545150	KO109B03-W37951	888	20	0.4	450	14	CD694156	CD694156
816	20	0.4	424	14	W37951	z613407.x1	889	20	0.4	451	13	BQ316711	BQ316711
817	20	0.4	425	10	BE779553	601464342	890	20	0.4	451	13	BQ349125	BQ349125
818	20	0.4	425	13	BQ349175	MR2-HT037	891	20	0.4	451	14	CA941572	CA941572
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820	20	0.4	426	10	BQ349287	MR2-HT037	893	20	0.4	452	13	BQ316700	BQ316700
821	20	0.4	427	14	CA950022	1T85902.Y	894	20	0.4	452	13	BQ316700	BQ316700
822	20	0.4	427	28	AZ490837	1M0324X06	895	20	0.4	452	13	BQ316700	BQ316700
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825	20	0.4	428	13	BQ349019	MR2-HT037	898	20	0.4	453	13	BQ316697	BQ316697
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837	20	0.4	434	13	BQ316714	PM0-CT032	910	20	0.4	455	13	BQ349011	BQ349011
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849	20	0.4	438	9	AA085885	z66h08.x	922	20	0.4	458	13	BQ349025	BQ349025
850	20	0.4	438	9	AA181603	aa13a08.Y	923	20	0.4	458	13	BQ349025	BQ349025
851	20	0.4	438	9	AA171801	z097c02.x	924	20	0.4	459	13	BM773346	BM773346
852	20	0.4	438	10	BE831945	QV4-MT006	925	20	0.4	459	13	BM773346	BM773346
853	20	0.4	438	12	BM689237	UT-E-CRO-	926	20	0.4	459	14	CA943297	CA943297
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864	20	0.4	442	12	BM756723	K-EST0035	937	20	0.4	464	13	BQ349052	BQ349052
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c 974	20	0.4	477	9	AV744797	AV744797 AV744797
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c 982	20	0.4	478	9	AA314480	AA314480 EST186356
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c 1000	20	0.4	486	14	CD804067	CD804067 UI-M-GVO-

## ALIGNMENTS

RESULT 1  
LOCUS CD653539 838 bp mRNA linear EST 18-JUN-2003  
DEFINITION AGNCCOURT 14542448 NIA Human H1 Embryonic Stem Cell cDNA Library  
(Long) Homo sapiens cDNA clone IMAGE:30420107 5', mRNA sequence.

ACCESSION CD653539  
VERSION CD653539.1 GI:11892045  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 838)  
NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Daniela S. Gerhard, Ph.D.

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Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Irene Gintis and Mahendra Rao, NIA  
cDNA Library Preparation: Yulan Piao and Minoru Ko  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC c  
http://image.lnl.gov  
Plate: NDMA495 row: m column: 12  
High quality sequence stop: 650.  
Location/Qualifiers  
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/note="Vector: PCMV-Sport6; Site 1: NotI; Site 2: SalI;  
This is a long-fragment enriched cDNA library (Genome  
Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01/  
cell line. Undifferentiated human ES cell line WA01/H1  
was obtained from WCell Research Institute, Inc.  
Madison, WI, cultured according to their instructions, on  
MEF feeders. They formed round colonies with defined edges  
and were positive for alkaline phosphatase, SSEA-4, OCT3,  
OCT4, REX1, URF, TERT, SOX2, CX43 and CX45. They are  
negative for GATA2, GATA4, PDX1, NCM, MSX1, FLT3, SSEA-1,  
TUBB3, NES, GFAP, and H0MES. When confluent, (18-10 days  
after plating), the ES cells from 4 x 6cm dishes were  
treated with 1 mg/ml collagenase, type IV  
(Invitrogen/GIBCO) for 5-10 min and gently scraped off  
with 5 ml pipette. RNA was purified with TRIzol Reagent  
from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558  
(2001). [PMID: 11544199] Double-stranded cDNAs were  
synthesized with an Oligo(dT) primer [Invitrogen:  
5'-pGACTAGTCTAGATCCGAGCGGCGCCCTTTTCTTTT-3'] from  
3.4g of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker lp-SalI, purified by phenol/chloroform  
extraction, and separated from free linkers by  
centrifugation 100 column. Then, the cDNAs were amplified by  
long-range high fidelity PCR using Ex Tag polymerase  
(Takara) with a primer SalI-S for 25 cycles. The products  
were purified by phenol/chloroform extraction and  
centrifugation 100 column. The cDNAs were digested with SalI  
and NotI enzymes and cloned into SalI/NotI site of  
pCMV-SPORT6 plasmid vector. The average insert size is  
about 3.6kb."

## ORIGIN

Query Match 11.2%; Score 637; DB 14; Length 838;  
Best Local Similarity 100.0%; Pred. No. 1.5e-284;  
Matches 637; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	3759	CGTGGCCGCTGCTAGTCTGCTTAACGCAAGTCCCGGAGAGTACCTCAGCTGGAAGCG	3818
DB	12	CGTGGCCGCTGCTAGTCTGCTTAACGCAAGTCCCGGAGAGTACCTCAGCTGGAAGCG	71
QY	3819	GCTGCAGATGCAATGCAACCTGAGATCCGCTGTGAGCTTGAAGTGAAGAGCTT	3878
DB	72	GCTGCAGATGCAATGCAACCTGAGATCCGCTGTGAGCTTGAAGTGAAGAGCTT	131
QY	3879	TGCGGAGCTGCAAGGAGATCCATGAGCTGAGTACCTGAGTGAAGCGGAGATCC	3938
DB	132	TGCGGAGCTGCAAGGAGATCCATGAGCTGAGTACCTGAGTGAAGCGGAGATCC	191
QY	3939	GTTCCGTGACATATAGACTTACACCATGCGGAGTGTGTTCCAGAAATGGAACACCC	3998
DB	192	GTTCCGTGACATATAGACTTACACCATGCGGAGTGTGTTCCAGAAATGGAACACCC	251



	Matches	613;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2683	AAGGTTGCTGGGCTGGAGATGTGAGGCGCTTTAGTGGATAGCTTAATCCCGAGAAACAGT	2742							
Dp	6	AAGGTTGCTGGGCTGGAGATGTGAGGCGCTTTAGTGGATAGCTTAATCCCGAGAAACAGT	65							
QY	2743	GTGTGTGAGATTGGGGAGAGCCAAAGCCAGCAGCATGACAGGCTTGAGAGATCTGCCTG	2802							
Dp	66	GTGTGTGAGATTGGGGAGAGCCAAAGCCAGCAGCATGACAGGCTTGAGAGATCTGCCTG	125							
QY	2803	GCTGTGTGTGGCCTGAAATTCATGCGCCGGTCTCAAGCTCTATTACTTATGACACTG	2862							
Dp	126	GCGTGTGTGGCCTGAAATTCATGCGCCGGTCTCTCAAGCTCTATTACTTATGACACTG	185							
QY	2863	ACTCTCTCAGATCTGAAAGCCAGCGCGGGGCCCATATCCGGAGGGAGCCCAAGTGCACAT	2922							
Dp	186	ACTCTCTCAGATCTGAAAGCCAGCGCGGGGCCCATATCCGGAGGGAGCCCAAGTGCACAT	245							
QY	2923	AAGAGGCCAACTGAATGCGGAGAGCAAGTGTGTGATTTTGGAAAGCAGCGCTGT	2982							
Dp	246	AAGAGGCCAACTGAATGCGGAGAGCAAGTGTGTGATTTTGGAAAGCAGCGCTGT	305							
QY	2983	CTCTTCCACAGGCGATCTCATCTCTCAATTGTCTGCAACACACATCTCGAGTAGAGTG	3042							
Dp	306	CTCTTCCACAGGCGATCTCATCTCTCAATTGTCTGCAACACACATCTCGAGTAGAGTG	365							
QY	3043	CTTAGAGTAGAAGTGTGCTGTGACAGTGGAGAGGGCCAAATCCACACAGAACTGGTCTTT	3102							

QY	3103	CAGTATGTGGAAGACCCACCATTGTCGGATTGAGCCAGAAATGAGACATTGTCAGTGA	3162
Db	426	CAGTATGTGGAAGACCCACCATTGTCGGATTGAGCCAGAAATGAGACATTGTCAGTGA	485
QY	3163	AACACACCCATCGCGCGATGTGGGGGACCCACTGTGACTCATACAGACCCCAGATCCGT	3222
Db	486	AACACACCCATCGCGCGATGTGGGGGACCCACTGTGACTCATACAGACCCCAGATCCGT	545
QY	3223	GCCAGCATTGAGGGAGAGACCATCATATCTGTGAGGTTCTGAGCGTACTGAGATG	3282
Db	546	GCCAGCATTGAGGGAGAGACCATCATATCTGTGAGGTTCTGAGCGTACTGAGATG	605
QY	3283	ACCTGTCAAGCGC	3295
Db	606	ACCTGTCAAGCGC	618

RESULT		3
LOCUS	AL707761	
DEFINITION	AL707761	483 bp mRNA linear EST 04-SEP-2003
ACCESSION	DKFPD66H2349.r1.666 (synonym: hlccl3)	Homo sapiens cDNA clone
VERSION	DKFPD66H2349.5,	mRNA sequence.
JOURNAL	AL707761	
COMMENT	AL707761.1 GI:19691116	
REFERENCE	EST.	
AUTHORS	Homo sapiens (human)	
TITLE	Homo sapiens	
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
	1.(baes 1 to 483)	
	Wambutic,R., Heuhner,D., Mewes,W., Weil,B. and Wiemann,S.	
	EST (Wambutic,R., Heuhner,D., Mewes,H.W., Weil,B. and Wiemann,S.)	
	Unpublished (1999)	
	Contact: MIPS	
	MIPS	
	IngoIsraedter landstr.1, D-85764 Neuherberg, Germany	
	This is the 5' sequence of the clone insert	
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;	
	sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing	
	consortium of the German Genome Project.	
	No sl sequence available.	
	This Clone (DKFPD66H2349) is available at the RZPD in Berlin.	

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..483

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686H2349"  
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/clone\_1ib="686 (synonym: hlc3)"  
/note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI; cDNA-collection"

## ORIGIN

Query Match 8.0%; Score 457; DB 9; Length 483;  
Best Local Similarity 100.0%; Pred. No. 7.4e-201;  
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2081 GAGTGAAGCTGCGCCGAGAGCTGCGCCGAGCTGCTGCGAGTGGAGCAAGATCCTGGTGGCCG 2140  
1 GAGTGAAGCTGCGCCGAGAGCTGCGCCGAGCTGCTGCGAGTGGAGCAAGATCCTGGTGGCCG 60  
2141 TGGAGGTATCAAGCTTATCAAGCTGAGAGCCCAAGAACTCTCCCAAGCCCAAGTCTGGGC 2200  
61 TGGAGGTATCAAGCTTATCAAGCTGAGAGCCCAAGAACTCTCCCAAGCCCAAGTCTGGGC 120  
2201 AGGCTGAGCTGAGATGCTATCTCAATCTCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2260  
121 AGGCTGAGCTGAGATGCTATCTCAATCTCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
2261 GCTTCAACAGCTCCAGCTGACAGTGCAGAGAACTCTTATCTTATGAGAGAGAGAGAGAGAG 2320  
181 GCTTCAACAGCTCCAGCTGACAGTGCAGAGAACTCTTATCTTATGAGAGAGAGAGAGAGAG 240  
2321 TCAACAGCTGCGCCGAGAGCTGAGAGTGCAGTGTGGAGATGGGCACTTCAACATTTGCAACC 2380  
241 TCAACAGCTGCGCCGAGAGCTGAGAGTGCAGTGTGGAGATGGGCACTTCAACATTTGCAACC 300  
2381 CAGCTGAGATTAAGTTTACCTCTCAAGTGTGGAGCCATGCTGAGAGCTGCGGCTGT 2440  
301 CAGCTGAGATTAAGTTTACCTCTCAAGTGTGGAGCCATGCTGAGAGCTGCGGCTGT 360  
2441 GCCTCAAGGCTGACCCAGATCTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2500  
361 GCCTCAAGGCTGACCCAGATCTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
2501 TGGCCAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2537  
421 TGGCCAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 457

RESULT 4 473 bp mRNA linear EST 04-SEP-2003  
EX645676  
LOCUS DKFZp781K1545.1 781 (synonym: hlc4) Homo sapiens cDNA clone  
DEFINITION DKFZp781K1545.1, mRNA sequence.  
ACCESSION EX645676  
VERSION EX645676.1 GI:34480009  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 473)  
Wamburt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Oeinger, A.,  
Fob, G., Han, M., and Wiemann, S.  
EST (Wamburt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Contact: MIPS  
COMMENT MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No sequence available.  
This clone (DKFZp781K1545) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

source

1..473

/organism="Homo sapiens"  
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/clone="DKFZp781K1545"  
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/lab\_host="DH10B"  
/clone\_1ib="781 (synonym: hlc4)"  
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## ORIGIN

Query Match 7.4%; Score 422; DB 13; Length 473;  
Best Local Similarity 99.8%; Pred. No. 1.4e-184;  
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3185 GAGCCCACTGAGACCTCATAGAGAACCCAGATCGGTGCGAGATGAGAGAGAGAGC 3244  
1 GAGCCCACTGAGACCTCATAGAGAACCCAGATCGGTGCGAGATGAGAGAGAGAGC 60  
3245 AATTAATATCTGAGAGTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 3304  
61 AATTAATATCTGAGAGTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 120  
3305 CTGTGGTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 3364  
121 CTGTGGTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 180  
3365 TGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 3424  
181 TGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 240  
3425 CGTGTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 3484  
241 CGTGTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 300  
3485 TCTTAAAGGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 3544  
301 TCTTAAAGGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 360  
3545 CTGTGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 3604  
361 CTGTGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420  
3605 AGTCCCACTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 3657  
421 AGTCCCACTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 473

RESULT 5 564 bp mRNA linear EST 22-JAN-2001  
BF953019  
LOCUS QV3-NN0198-111100-373-h10 NN0198 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BF953019  
ACCESSION BF953019.1 GI:12370294  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 564)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Bruneir, A., deoliveira, P.S., Bucher, P., Jongsneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Stimpson, A.J. Sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE  
20202663  
PUBMED  
10737800

COMMENT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
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Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV3&t2=QV3-NN0198-  
11100-373-1108c3-2000-11-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 586.  
Location/Qualifiers  
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/dev\_stage="Adult"  
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/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 5.8%; Score 328; DB 10; Length 564;  
Best Local Similarity 100.0%; Pred. No. 8.6e-141; Indels 0; Gaps 0;  
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGGCGATGCGCTGGAGCTGACCTGCTCTCTCCACCTCTCTATGTTGGGATG 60  
234 ATGAAGGCGATGCGCTGGAGCTGACCTGCTCTCTCCACCTCTCTATGTTGGGATG 233  
61 GGCTCTCTCACTTTGGTCACTCCGAGCAGCCCGCTGCTCCAGAGCAGCGTCAATT 120  
294 GGCTCTCTCACTTTGGTCACTCCGAGCAGCCCGCTGCTCCAGAGCAGCGTCAATT 353  
121 GTTCACTTTCCGAGAGAGCCCGCGAGGTTTCAATCACTCTGTTGGTGGATGAGAGACA 180  
354 GTTCACTTTCCGAGAGAGCCCGCGAGGTTTCAATCACTCTGTTGGTGGATGAGAGACA 413  
181 GGAACATTACTTGGGGGCGCTCATGCGATTTCAGAGCTCTCAGGAGCTTGAAGTTC 240  
414 GGAACATTACTTGGGGGCGCTCATGCGATTTCAGAGCTCTCAGGAGCTTGAAGTTC 473  
241 TTGGTATCGCATGAGACAGAGGCGCGAGCAGACAAACCCCAAGTTACCCACCCGATC 300  
474 TTGGTATCGCATGAGACAGAGGCGCGAGCAGACAAACCCCAAGTTACCCACCCGATC 533  
301 GTCCAGAGCTGCAGATGAGCCCTGACCA 328  
534 GTCCAGAGCTGCAGATGAGCCCTGACCA 561

RESULT 6  
BF952116/c 512 bp mRNA linear EST 22-JAN-2001  
LOCUS BP952116  
DEFINITION CVI-NN0229-101100-445-e08 NN0229 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF952116

VERSION BF952116.1 GI:12369391  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Golman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Stimpson, D.H.,  
Bruneir, A., deoliveira, P.S., Bucher, P., Jongsneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Stimpson, A.J.

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL  
MEDLINE  
20202663  
PUBMED  
10737800

COMMENT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV3&t2=QV3-NN0229-  
101100-445-e08&t3=2000-11-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 512.  
Location/Qualifiers  
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/dev\_stage="Adult"  
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/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 5.5%; Score 313; DB 10; Length 512;  
Best Local Similarity 99.7%; Pred. No. 8e-134; Indels 1; Gaps 0;  
Matches 363; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5322 GGCTCAGACCTTCATGAGCTCTTCTCCAGCTCAGAGCAGCGCTGGCAGAGCTTGGCC 5381  
496 GGCTCAGACCTTCATGAGCTCTTCTCCAGCTCAGAGCAGCGGTGGGCAAGAGCTGGCC 437  
5382 GTCCAGAGAGTGTGATGATGAGCAGAGCAGTCCCGAGTCAAGAGTGGTGGAGAGTA 5441  
436 GTCCAGAGAGTGTGATGATGAGCAGAGCAGTCCCGAGTCAAGAGTGGTGGAGAGTA 377  
5442 TTACTGAGACATAGGAGAGATGAGCAGCATCAGGACCAAGACATGAAAGCATPCTTGGC 5501  
376 TTACTGAGACATAGGAGAGATGAGCAGCATCAGGACCAAGACATGAAAGCATPCTTGGC 317  
5502 TTAGAGAGTCCCGAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5561  
316 TTAGAGAGTCCCGAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 257  
5562 CTCTTATGTGGGCAATPACAGCGAGAGATCTTGGACTCTTGGACCAAGATGACAGATG 5621  
256 CTCTTATGTGGGCAATPACAGCGAGAGATCTTGGACTCTTGGACCAAGATGACAGATG 197



QY 4109 GCACGCTTGAAGTCCAGGCTAGCTTCCATGCC 4143  
 DB 53 GCACGCTTGAAGTCCAGGCTAGCTTCCATGCC 19

RESULT 9  
 LOCUS AA077578/c  
 DEFINITION 251 bp mRNA linear EST 24-SEP-1999  
 7B19H10 Chromosome 7 Fetal Brain CDNA library Homo sapiens CDNA  
 clone 7B19H10, mRNA sequence.  
 AA077578  
 AA077578.1 GI:1837052  
 EST.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 251)  
 Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L.,  
 Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, B.D.  
 2006 expressed-sequence tags derived from human chromosome  
 7-enriched cDNA libraries  
 Genome Res. 7 (3), 281-292 (1997)  
 97228905  
 9074931

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

Contact: Eric D. Green  
 Genome Technology Branch  
 National Human Genome Research Institute/NIH  
 49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892  
 Tel: 3014020201  
 Fax: 3014024735  
 Email: egreen@bgrl.nih.gov  
 Plate: 19 row: H column: 10  
 Seq primer: -21M13 (ABI).  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="7B19H10"  
 /sex="female and male mixture"  
 /tissue\_type="brain"  
 /dev\_stage="pool of 9 week and 12 week"  
 /lab\_host="B. coli strain DHS alpha"  
 /clone\_lib="Chromosome 7 Fetal Brain CDNA Library"  
 /note="Organ: brain; Vector: pAMP10; CDNA was generated  
 from cytoplasmic RNA using a mixture of random DNA  
 hexamers and oligo(dT). From this pool of CDNA, human  
 chromosome 7-enriched cDNA was isolated by direct cDNA  
 selection using chromosome 7 genomic DNA (cosmids). The  
 resulting direct-selected cDNA was cloned into a plasmid  
 vector using a non-directional uracil DNA glycosylase  
 (UDG)-mediated cloning strategy."

ORIGIN  
 Query Match 3.6%; Score 206; DB 9; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 4e-84;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 CCCCCGAGTTGCGTCGAGATGAAGAGTGTCCGCTGACGGTCCATCCCAACAT 1701  
 DB 206 CCCCCGAGTTGCGTCGAGATGAAGAGTGTCCGCTGACGGTCCATCCCAACAT 147  
 QY 1702 ATCTCGCTCTCACTACCAAGTGTCTGTCTGTCTGAGAGCTACATGTCCCGAGCTG 1761  
 DB 146 ATCTCGCTCTCACTACCAAGTGTCTGTCTGTCTGAGAGCTACATGTCCCGAGCTG 87  
 QY 1762 TCAGCTGGGCTCACTGACGCTTTGAGAGCTGTGACAGATGAGATGGGCTGGTGGTGGC 1821  
 DB 86 TCAGCTGGGCTCACTGACGCTTTGAGAGCTGTGACAGATGAGATGGGCTGGTGGTGGC 27  
 QY 1822 AATCAGATCCAGTGTACTCCCTGC 1847

DB 26 AATCAGATCCAGTGTACTCCCTGC 1

RESULT 10  
 LOCUS BF953008/c  
 DEFINITION 493 bp mRNA linear EST 22-JAN-2001  
 QV3-NN0198-111100-373-b07 NN0198 Homo sapiens CDNA, mRNA sequence.  
 BF953008  
 BF953008.1 GI:12370283  
 EST.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 493)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.R., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.U.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

Contact: Simpson, A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL:  
 (http://www.ludwig.org.br/bcrlpcts/gethtml2.pl?fl=QV3&c2=QV3-NN0198-  
 111100-373-b07&c3=2000-11-11&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 493.  
 Location/Qualifiers  
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 /clone\_lib="NN0198"  
 /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN  
 Query Match 3.5%; Score 198; DB 10; Length 493;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-80;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCCATGCGCCCTGGAAGTGAAGTCTCTCTCCACCTCTCTCAATGTTGGCATTG 60  
 DB 278 ATGAAGCCATGCGCCCTGGAAGTGAAGTCTCTCTCCACCTCTCTCAATGTTGGCATTG 219  
 QY 61 GGCTCTCTCACTTTGCTCAACCCGCGGAGCCAGCCCGCTGTCCAGAGAGAGCGGCTATT 120  
 DB 218 GGCTCTCTCACTTTGCTCAACCCGCGGAGCCAGCCCGCTGTCCAGAGAGAGCGGCTATT 159  
 QY 121 GTCAATTCGAGAGAGAGCCCGCGGAGGTTTCATCACTGTGTGTGATGAGAGACA 180  
 DB 158 GTCAATTCGAGAGAGAGCCCGCGGAGGTTTCATCACTGTGTGTGATGAGAGACA 99  
 QY 181 GGAACATTTACTTGGGG 198

Db 98 GGACACATTACTGGGG 81

RESULT 11  
LOCUS BF312056/c 924 bp mRNA linear EST 21-NOV-2000  
DEFINITION 601897930F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4127359 5', mRNA sequence.

ACCESSION BF312056  
VERSION BF312056  
KEYWORDS BF312056.1 GI:11259847  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 924)  
NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at: Image.lnl.gov  
Plate: L10M1018 row: K column: 08  
High quality sequence stop: 657.  
Location/Qualifiers  
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/tissue\_type="neuroblastoma"  
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/clone\_lib="NIH MGC 19"  
/note="Organ: brain; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

ORIGIN

Query Match 3.1%; Score 176; DB 10; Length 924;  
Best Local Similarity 100.0%; Pred. No. 5.7e-70;  
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GGCCAAGTCCACAGAGACCTGCTCTTCAGTATGGAAGACCCCACTCTGGCGAT 3134  
DB 331 GGCAGATTCACAGAGACCTGCTCTTCAGTATGGAAGACCCCACTCTGGCGAT 272  
QY 3135 TGAAGCAGATGAGCATTTGCTGAGAAACACCCATGCGGTATGGGGACCACT 3194  
DB 271 TGAGCCAGATGAGCATTTGCTGAGAAACACCCATGCGGTATGGGGACCACT 212  
QY 3195 GGACCTATATACAGACCCCGAGATCCGCGCAACATGAGGGAGAGACATCA 3250  
DB 211 GGACCTATATACAGACCCCGAGATCCGCGCAACATGAGGGAGAGACATCA 156

RESULT 12  
LOCUS AA077496 242 bp mRNA linear EST 24-SEP-1999  
DEFINITION 7818311 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7818311, mRNA sequence.

ACCESSION AA077496  
VERSION AA077496.1 GI:1836570

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 242)  
Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D., 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries  
Genome Res. 7 (3), 281-292 (1997)

JOURNAL MEDLINE  
PUBMED 9728905  
5074931  
COMMENT Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Plate: 18 row: G column: 11  
Seq primer: -21M13 (AB1).  
Location/Qualifiers  
1..242  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="7818311"  
/sex="female and male mixture"  
/tissue\_type="brain"  
/dev\_stage="pool of 9 week and 12 week"  
/lab\_host="E. coli strain DH5 alpha"  
/clone\_lib="Chromosome 7 Fetal Brain cDNA library"  
/note="Organ: brain; Vector: PAMPI0; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

ORIGIN

Query Match 2.7%; Score 156; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 7.4e-61;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2720 GTTACATCCCTGCAGACAGATCGTGTGTGATGGGGAGGCCAGCCAGCAGCATG 2779  
DB 87 GTTACATCCCTGCAGACAGATCGTGTGTGATGGGGAGGCCAGCCAGCAGCATG 146  
QY 2780 CAGGCTTGTTGAGATCTGCGTGTGTGTGCTGCGCTGAAATTATGAGCCCGGTCTCAC 2839  
DB 147 CAGGCTTGTTGAGATCTGCGTGTGTGTGCTGCGCTGAAATTATGAGCCCGGTCTCAC 206  
QY 2840 AGCTCTATTACTGATGACACTGACTCTCTCAGATC 2875  
DB 207 AGCTCTATTACTGATGACACTGACTCTCTCAGATC 242

RESULT 13  
LOCUS BG216679 789 bp mRNA linear EST 21-APR-2001  
DEFINITION R8736373 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG216679  
VERSION BG216679.1 GI:13742700  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 789)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

FEATURES	source	location/Qualifiers
JOURNAL	Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikis, A., Hesse, J., Cotner, K., Lo, K., Offenbacher, J., Danzig, J., and Ducat, M.	
MEDLINE	Creation of genome-wide protein expression libraries using random activation of gene expression	
PUBMED	Nat. Biotechnol. 19 (5), 440-445 (2001)	
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@atersys.com High quality sequence stop: 456. Location/Qualifiers 1..789 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_lib="Athersys RAGE Library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', the Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."	
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Query Match	2.7%; Score 152; DB 12; Length 789;	
Best Local Similarity	100.0%; Pred. No. 8..le-59;	
Matches 152; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Y	2862 GACTCTCTCAGATCGAAGCCACGCGGGGAGCCATGTCGAGAGGACCAAGTACCAT	29211
Db	356 GACTCTCTCAGATCGAAGCCACGCGGGGAGCCATGTCGAGAGGACCAAGTACCAT	415
Y	2922 CACAGGACCAACTGAATGCCGGAAGCACGTGTGTGATTTGGAAAGCAGCCCTG	2981
Db	416 CACAGGACCAACTGAATGCCGGAAGCACGTGTGTGATTTGGAAAGCAGCCCTG	475
Y	2982 TCTCTTCACAGAGCGATCTCATCTTACATG 3013	
Db	476 TCTCTTCACAGAGCGATCTCATCTTACATG 507	
RESULT 14		
T07763/c	328 bp mRNA linear EST 30-JUN-1993	
LOCUS	EST05653 Fetal brain, StrataGene (cat#336206) Homo sapiens CDNA	
DEFINITION	clone HFBEN78, mRNA sequence.	
ACCESSION	T07763	
VERSION	T07763.1 GI:318912	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 328) Adam, M.D., Keryavag, A.R., Fields, C. and Venner, J.C. 3,400 expressed sequence tags identify diversity of transcripts from human brain Nat. Genet. 4, 256-267 (1993)	
JOURNAL	93364420	
MEDLINE	8358434	
COMMENT	Contact: Adams, MD The Institute for Genomic Research 932 Clapper Road, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: mdadams@tigr.org	

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FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
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        /clone="HPBEN78"
        /clone_1b="Fetal brain, Stratagene (cat#936206)"
        /note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
        oligo-dT + random primed cDNA synthesis; lambdaZAP-II
        vector, 1.0kb average insert size."
ORIGIN
  Query Match      2.2%; Score 123; DB 14; Length 328;
  Best Local Similarity 100.0%; Pred. No. 1,9e+45;
  Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4751 TGGCCCACTCCAGGTCGCCAGATGATGTCGCGTGGTGGCATTAAGTCCAGAGGTGACAG 4810
Db 172 TGGCCCACTCCAGGTCGCCAGATGATGTCGCGTGGTGGCATTAAGTCCAGAGGTGACAG 113
QY 4811 CCTATAACGACGTGAACAACCTCCACCGCTCTCCAGACCTCAGCAAGTAAATATGAAAAA 4870
Db 112 CCTATAACGACGTGAACAACCTCCACCGCTCTCCAGACCTCAGCAAGTAAATATGAAAAA 53
QY 4871 TGA 4873
Db 52 TGA 50
RESULT 15
LOCUS AA076688 302 bp mRNA linear EST 24-SEP-1999
AA076688 7803G05 Chromosome 7 Fetal Brain cDNA Library Homo sapiens CDNA
Accession clone 7803G05, mRNA sequence.
AA076688
AA076688.1 GI:1836316
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 302)
Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,
Robbins,C.M., Nusbaum,J.C., Lovett,M. and Green,E.D.
2006 expressed-sequence tags derived from human chromosome
7-enriched cDNA libraries
Genome Res. 7 (3), 281-292 (1997)
97288905
9074931
Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Plate: 03 row: G column: 05
Seq primer: -21M13 (ABI).
FEATURES
  source
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="7803G05"
        /sex="female and male mixture"
        /tissue_type="brain"
        /dev_stage="pool of 9 week and 12 week"
        /lab_host="E. coli strain DH5 alpha"
        /clone_11b="Chromosome 7 Fetal Brain cDNA Library"
        /note="Organ: brain; Vector: pMP10; cDNA was generated
        from cytoplasmic RNA using a mixture of random DNA

```

hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

## ORIGIN

```
Query Match      2.1%; Score 118; DB 9; Length 302;
Best Local Similarity 99.1%; Pred. No. 3.9e-43;
Matches 218; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1725 GCTGCTGCTGCTGAGAGCTACATGTCCCGAGCTGTCAAGTGGCGTCACTGCACCTT 1784
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Db 83 GCTGCTGCTGCTGAGAGCTACATGTCCCGAGCTGTCAAGTGGCGTCACTGCACCTT 142

QY 1785 TGAAGACCTGTCAAGATGATGGCTGGTCTGGGCAATCAAGTCAAGTGGCTACTCCCC 1844
    |||
Db 143 TGAAGACCTGTCAAGATGATGGCTGGTCTGGGCAATCAAGTCAAGTGGCTACTCCCC 202

QY 1845 TGCAGCCCAAGAGAGTGCCTCGATCATCAAGAAATGGGAGCCACCATGTGTACAGCT 1904
    |||
Db 203 TGCAGCCCAAGAGAGTGCCTCGATCATCAAGAAATGGGAGCCACCATGTGTACAGCT 262

QY 1905 TCAGCTCAATCAAGAGAGCCCGCATGACCTTCGCCAGC 1944
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Db 263 TCAGCTCAATCAAGAGAGCCCGCATGACCTTCGCCAGC 302
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Search completed: February 20, 2004, 09:34:27  
Job time : 8811 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 16:32:38 ; Search time 27 Seconds

(without alignments)  
2971.162 Million cell updates/sec

Title: US-09-964-956-13

Perfect score: 9990  
Sequence: 1 MKAFMWTCLLSHLLWGM.....QKAYKLEQVITLMSLSNKK 1896

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349	13.5	1568	3	US-09-181-706-2
2	1349	13.5	1568	3	US-09-456-791-2
3	1349	13.5	1568	3	US-09-459-066-2
4	1349	13.5	1568	4	US-09-459-065-2
5	538.5	5.4	1404	4	US-09-345-473E-24
6	308	3.1	607	4	US-08-556-422A-4
7	263	2.6	888	4	US-09-077-940A-4
8	244.5	2.4	887	4	US-09-077-940A-2
9	227	2.3	724	1	US-08-121-713D-62
10	227	2.3	724	1	US-08-835-268-62
11	227	2.3	724	2	US-09-060-692-62
12	227	2.3	724	2	US-08-833-391-62
13	227	2.3	724	4	US-09-060-610-62
14	227	2.3	724	5	PCT-US94-10151A-62
15	207	2.1	730	1	US-08-121-713D-58
16	207	2.1	730	1	US-08-835-268-58
17	207	2.1	730	2	US-09-060-692-58
18	207	2.1	730	3	US-08-833-391-58
19	207	2.1	730	4	US-09-060-610-58
20	207	2.1	730	5	PCT-US94-10151A-58
21	200	2.0	771	1	US-08-121-713D-54
22	200	2.0	771	1	US-08-835-268-54
23	200	2.0	771	1	US-09-060-692-54
24	200	2.0	771	3	US-08-833-391-54
25	200	2.0	771	4	US-09-060-610-54
26	200	2.0	771	5	PCT-US94-10151A-54
27	196.5	2.0	655	4	US-08-556-422A-3

28	186	1.9	712	1	US-08-121-713D-64	Sequence 64, Appl
29	186	1.9	712	1	US-08-835-268-64	Sequence 64, Appl
30	186	1.9	712	2	US-09-060-692-64	Sequence 64, Appl
31	186	1.9	712	3	US-08-833-391-64	Sequence 64, Appl
32	186	1.9	712	4	US-09-060-610-64	Sequence 64, Appl
33	186	1.9	712	5	PCT-US94-10151A-64	Sequence 64, Appl
34	185	1.9	650	1	US-08-121-713D-60	Sequence 60, Appl
35	185	1.9	650	1	US-08-835-268-60	Sequence 60, Appl
36	185	1.9	650	2	US-09-060-692-60	Sequence 60, Appl
37	185	1.9	650	3	US-08-833-391-60	Sequence 60, Appl
38	185	1.9	650	4	US-09-060-610-60	Sequence 60, Appl
39	185	1.9	650	5	PCT-US94-10151A-60	Sequence 60, Appl
40	178	1.8	930	4	US-09-254-594-6	Sequence 6, Appl
41	177.5	1.8	929	4	US-09-254-594-3	Sequence 3, Appl
42	174.5	1.7	862	4	US-08-556-422A-2	Sequence 2, Appl
43	147	1.5	666	3	US-09-240-410-2	Sequence 2, Appl
44	146.5	1.5	606	3	US-09-041-236-4	Sequence 4, Appl
45	146.5	1.5	606	4	US-09-771-467C-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-181-706-2  
Sequence 2, Application US/09181706  
Patent No. 6130068  
GENERAL INFORMATION:  
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
APPLICANT: Robert F. Dubose, Richard S. Johnson  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09181,706  
FILING DATE: October 28, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/958,598 (converted to a  
APPLICATION NUMBER: Provisional, see below)  
FILING DATE: October 28, 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: --to be assigned-- (US98 08/958,598  
APPLICATION NUMBER: conversion to Provisional application)  
FILING DATE: October 26, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)253-0644  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-181-706-2

Query Match 13.5%; Score 1349; DB 3; Length 1568;  
 Best Local Similarity 24.8%; Pred. No. 9.6e-112; Indels 576; Gaps 74;  
 Matches 480; Conservative 291; Mismatches 591;

Db 72 YKLSDDIKVLTHTGTGDEDNPKCYPPRIYVOTCNEPLITT-----NNVAKLLIDYK 123  
 70 YLSEHSISRLYRDQAG-----NCTEPVSLAPAPRPRDSSFSK-LLLPYR 113

Qy 124 ENR-----LIACSLVGTGCKLRLDPLFGSEPKHEHYLSGV-----NNGSGVGV 172  
 114 EGAAGLGGLLTGTFDGRACEVRLGNL-----SRNSLRGTEVSCHQGSGTAGV 165

Qy 173 IVSYNLDLKLPIA-----TAVDGKPEYPTISRKLTGNS 208  
 166 VYR-AGRNRMWYLAVALTYVLPEPETASRCNPASDHDIALKDTGSLAQELGRLK 224

Qy 209 EADGMFAVYHDEYV-ASMKIISDPTITLFDITLYYVGFSSGNFYFILTQPEVSP 267  
 225 LCEGAGSLHFVDAFLMNGSIYFP-----YYPNTTSG-----AATGWSMARIA 268

Qy 268 GSTTKEGYTSTKLVLCKEDTAFNSYVEVPICERSGVE-YRLQAAYLKAGAVLGRTL 326  
 269 GST-----EVLFGG-QASLDGCHGHPDGRLLSSLSVEA-----302

Qy 327 GVHPPDDLFTVFS--KGQKRNKSLDSALCITLKQINDRIKERLQSCYRGEGLTDLA 384  
 303 -----LDVMAGVFSAAAGEGERSPTTTALCLFRMSEIQAFAR-----VS 344

Qy 385 W-LKVKDIPCSSALLITIDNFCGLDMNAPLGVSDMVGIPFETEDRMTSVIAYYKNH 443  
 345 WDFPTEHSEKGE-----DQP-----ERVQIASSTLIHDLISVGTVMNR 387

Qy 444 SLAVGTGSKGLKIRVDGRGNALQYETVOV-----DGYLRDMASKO 490  
 388 TLFVFGTGDGQLLKYL-----GENLTSNCPVYIIEKEPTVFYKLVDPDV-----K 435

Qy 491 HEOLYKSEBOLTVPVESCGOYSCGCLSGADPHGCMCVLAHTCTRKEXCERKERR 550  
 436 NIYITLTGKEVRRIRVANCKNKSCECLTATPHGCMCHSLDRCTFGQDC-----487

Qy 551 FASEMKQCVRLTVHNNISVSQYVNLVLETYVPELSAGVNTCEDLSEMDGLVGNQI 610  
 488 -----VSENLLE-----NMLDISSG-----502

Qy 611 QCYSPAKEVERITENDGHHVLOLQSKXETGMPFSTSFVFNCSYVNSCL-SCYESP 669  
 503 -----AKCPKI-----QIIRSSKEKTVTMVGSF-----SPRHSKCMKAVNDS 542

Qy 670 YCHWCKYRHVCTHDPTCSFOQGRVKLPEDCPOLLRVDKLLVVEVYIKPITLAKKLPQ 729  
 543 -----RELQ-----QKSKQ 551

Qy 730 PQSGRGVECLINTGSGFORVPALRFNSSVQCQNTSYSEGMELNLPVELTYVNN--G 787  
 552 PRR-----TCTCSI-----PTATYKDVSVVWVNFSGS-----KMLSD 585

Qy 788 HFNINDPAONKVLTKCGAMESCGCLKADPFCAGWCQGGPQCTLRQHCPAGEOSMLE 847  
 586 RNFNTN-----CSLKE-CPACVET-----GCAMCKSARAC-----615

Qy 848 LSGAASKCTNPRITELIIPYTGREGTGYTIRGENLGLFPDIASHVYVAVEGSLVDG 907  
 616 -----IHPTA-----CDP-----S 625

Qy 908 YIPAEQIVCEM-----GEAKPSQAHGVEICVACRPEFARSSQLYFMTLTSLDKP 961  
 626 DYERHQEQCPAVERKTSGGGRPKENKG-----NRNQALQVRY-----IKSIEP 669

Qy 962 SHGPMSSGGTQVITITGNLNAGSNV-VWFGKQPC-----LFHRSPEYIYCNSTSDSEV 1014  
 670 QKVSSTLGSKNVIVTGANFTRASNTIMILKGTSTCDKDVIVQSHVLTNDHMKFSLPSRK- 728

Qy 1015 IEMK-VSQVDRAKIHQDLVQYVEDPTIVRIEBEWSIVSGNTPJAVGTHLDLQNDQI 1073  
 729 -EMROVCIQFDGNCSSVGLSLYIALPHCSLIFPATWISGQNTMMGRNFVIDN--L 785

Qy 1074 RAKGCKKHINICEVLTNTEMTQCAPALALGPDHQSDLTERPEBEGFLDNDVQSLILNK 1133  
 786 IISHELKNINSECVATYCGFLAPSL-----KSKRTVYTKLRQD 830

Qy 1134 T-----NFTYYPNPVFEAFGSPGILELKPPTIILKGNLLPVAAGNVKLTNTVAGEK 1188  
 831 TYLDGGLTQYREDPRFTGYR-----VESEVDELEVKIQ-----KENDNENISK 875

Qy 1189 PCTTVV---SDVQLCESPNLI-----GRKHWARQWCMYS 1222  
 876 DIEITLIFGEGNQLNCSFENRTNODLTTLCKIKGTASTIANSKKVRKGNLE-- 933

Qy 1223 PGWVYIAPDS-PLSLPAIVSIAVAGLLIFIVAVLIAKERSRESDDLTLRLQWQMDNL 1281  
 934 ---LYVEGSAVSPTWYFVLVLPV---LVIYIIPAAGVTRKSKXK-LSRKQSQ-QLELL 984

Qy 1282 ESRVALCEKAPAEIQTDIHELTSDDLQAG-IPPLDYRTYMKVLPF--GIEDHPLARDL 1338  
 985 ESELKEIRIDGFABEQMDKLDV---VDSFGTVPLDYGHFALRFFPESGGFTLFTEDM 1041

Qy 1339 EVPGYRQERVEKGLKLPF--QIINNKFLLSFIRTLJESQSFMSRDRGNVASLMTVLQS 1396  
 1042 ---HNRANDKNESLTHLDALICNKSFLVYIHTLEKQNPVADRLFASFLTALQT 1097

Qy 1397 KLEIATDVIKQILLADIDKNLESKNHFKLLRRTESVAEKULTWFTLLKFLKECGGE 1456  
 1098 KLVYLTSLIEVLTPLIMEQC--SNMQPLMLRRRESVEKLLTMMWSVCLGFLFETVE 1155

Qy 1457 PLFSLFCALKOOMEKGPIDALNGEARYSGISEDKLIRQIDYKTVLSCV---SPDNANSP 1513  
 1156 PLYLLVTTLNQKINGPVVDITCKLYTLNEDMLMOPPESTVALNVFEKIPNEBAD 1215

Qy 1514 ---EVPVKILNCDITTOVEKILDAIFKNVPCSHRPKAADMDLEWQSGAMILQDEDI 1570  
 1216 VGRNISVANVLDGDTIQAKKEKIFQAFLSKNGSPYQIQLNEIGLEIOMGTROKELLIDDS 1275

Qy 1571 TKIKENDKRLNTLHAYQVDPQSGVVALYSKQVTANAVNSVRSATSKYENMIRYGS 1630  
 1276 SVILEGTYKLTIGHTEISNGSTIKV-----FKIANFTSD 1312

Qy 1631 PDLRSRPTMTTPDLESGYKMHLYKNHEHQDQEGDSGR--WVSEIYLRLLATKGTL 1688  
 1313 VEYSDHCHLLPDESA-----FQVQGRKH-----RGKHFKYKEMYLFTLLSTKVAI 1361

Qy 1689 QKRVDDLFEITISTARGLALPLAKMFDPLDEQADKHGHDHVRHWNKSNCLPLRFW 1748  
 1362 HSYLEKLFERSIMSLPR--SRAPFAIKYFPDFLDADLENKKITDPVVAHIWKTNSLPLRFW 1419

Qy 1749 VNMKINQCFVFDIHKNSITDACISVAQTFMDSCTSEHRLKQDSPSKLVIYAKDIPSYK 1808  
 1420 VNILKNQCFVFDIKRPHDGLCLSVIQAQFMDAFSLTEGQJKEKAPTNLLVAKXIPYK 1479

Qy 1809 NMYERYSDIGKMPAISDDQNNAYILABQSRMMEFNMSALSELFSYVGKXSEBILGFL 1868  
 1480 EBYKSYKAIKRLPLSLSSSEMEEFLOESKRNHEFNEVALTELTKYIKVIFDELANKL 1539

Qy 1869 DHD---DQCKOKLAVKL 1883  
 1540 EREGGLEAOKQDLNKHV 1557

Db 1540 EREGGLEAOKQDLNKHV 1557

RESULT 2  
 US-09-458-791-2  
 ; Sequence 2, Application US/09458791  
 ; Patent No. 6174689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Spriggs, Melanie  
 ; TITLE OF INVENTION: VIBRAL ENCODED SEMAPHORIN PROTEIN  
 ; RECEPTOR DNA AND POLYPEPTIDES

NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Janis C. Henry  
 STREET: 51 University St.  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: US  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS/Windows 95  
 SOFTWARE: Word for Windows 95, 7.0a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/458,791  
 FILING DATE: 10-Dec-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/958,598  
 FILING DATE: 28-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Henry, Janis C  
 REGISTRATION NUMBER: 34,347  
 REFERENCE/DOCKET NUMBER: 2631  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)470-4189  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1569 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-458-791-2  
 Query Match 13.5%; Score 1349; DB 3; Length 1568;  
 Best Local Similarity 24.8%; Pred. No. 9,6e-112;  
 Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;  
 QY 72 YKLSIDLKLVTHETGPEEDNPKCYPRIVQYCNBPLTTT-----NNVKKMLIDYK 123  
 DB 70 YLEHSLSLRYDQAG-----NCTEPVSLAPPARPPSSPSK-LLELYR 113  
 QY 124 ENR-----LIACGLSYGICLKLELDFKLGEPYHKKEHLSGV-----NESSVGV 172  
 DB 114 EGAAGLGGLLTGWTFDRGACEVRPLGNL-----SNSLRNGTEVVSCHPQGSTAGV 165  
 QY 173 IYSVSLDDKLFIA-----TAVDGKPEYFPITISSRKLTKNS 208  
 DB 166 VVR-AGRNRRWYLAVAATYVLRPEPTASRCNPASDHDTALAKOTEGRSLATQELGLK 224  
 QY 209 EADGFAFYFHDEYV-ASMIKIPSDFTFTIIPFDIYYGSSGNFVFLTLQPMVSP 267  
 DB 225 LLEGAGSLHFVAFMNGSIYFP-----YFPNYTSG-----AATGMPMAMIA 268  
 QY 268 GSTTKEQVYTSKLVKCKEDTAFNSYVEVPICSGSGVE-YRLQAAYSKAGAVLGRTL 326  
 DB 269 QST-----EVLFGG--QASLDGCHPDGRRLSLSSSIVEA----- 302  
 QY 327 GVAHPDDLLFTVFS--KQGRKRRKSIDESALCIFIILQINDRIKERLQSCYRSGSTLDA 384  
 DB 303 -----LDVWAGVFAAAGGERSPTTALCLFRMSEIOARAKR-----VS 344  
 QY 385 W-LKVDIDCSSALLIIDNFCGLDMKAPLGVSDMVRGIFPTEDRDRTSYIAVYKQH 443  
 DB 345 WDFKTESKCKES-----DQF-----ERVQPIASSTLIHSDLTSYGGVWNR 387  
 QY 444 STAFVGTSGKGLKIRIVDGRGNALQYETVQV-----DQGVLRDMAFSKD 490  
 DB 388 TVLFLTGQGLKVLIL-----GENLTNSCPVYVEIKETPVFYKLVDPDV-----K 435  
 QY 491 HEGLIYMSRQLTRVAVESGGYQSGCEGLSGSDPHCGWCVLHNTCTRKRERESKEPRR 550

DB 436 NIYIYLLAKGEVRIIRVANONCKHKSCECLTATDPHCGCHSLQRCCTFGDC----- 487  
 QY 551 FASEMKQCVRLVYHPNNISVSQYNTLVLETYNVPELSAGVACTPEBLSBMGLVYVNGQ 610  
 DB 488 -----VHSENLE-----NWDLISSG----- 502  
 QY 611 QCSPPAKEVPRITITENGDDHVVQLKSKETGMPFASFPFYNSVANSCL-SCVESP 669  
 DB 503 -----AKCQPKL-----QIRSSKEKTYTMVGSF-----SPRSKGVKRVDS 542  
 QY 670 YRCHMCKYRHVCTHDPKTSFQEGRYKLPEDCPQLRVDKILVPEVIVPITLKAQLPQ 729  
 DB 543 -----RELCL-----ONKSQ 551  
 QY 730 PQSGRGVECTINIQSGEQRVAPALRFNSSSVOCQNTSYSGEWEINLPLELTVVNR--G 787  
 DB 552 ENR-----TCTGSI-----PTRAYDVSVVNMVPSFGS-----WNLSD 585  
 QY 788 HFNIDNPAONKXVLYCGAMRESQGLCLADPDPAFCGCGPQCTLRQCPAQSQMLE 847  
 DB 586 RFNFTN-----CSSLKE-CPACVET-----GCAMCKSARRC----- 615  
 QY 848 LSGAKKCTNPRTEILIPVTGREGGTXITIRGENGLFPRDIASHVYKAVGECSPLYDG 907  
 DB 616 -----LHPFLTA-----CDP--S 625  
 QY 908 YIPAEQIVCEM-----GEAKPSQAHAFVEICVAVCRPEFMARSGLYYFMTLTSCLKP 961  
 DB 626 DYERNQEQCPVAVEKTSGGGRPKNG-----NRTQALQVY-----IKSIBP 669  
 QY 962 SRGPMGGTQYITTGNNLAAGSV--VVMFGKQPC-----LPHRBSPTIYCNSTSSDV 1014  
 DB 670 QKVSTLGKSNVITYGAFPRASNTWLKSTGCDKQVIOVSHVLDTHMKTSLSPSRK 728  
 QY 1015 LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPMISVSGNTPFIAMGTHLDLIQNPQ 1073  
 DB 729 -EMKDVCIQPDGNGCSVSLSYIALPHCSLIPPAATWISGQNTIMGRNFVIDN--L 785  
 QY 1074 RAVGGKEHINICEVLANIEMTQAPALALGPBHQSDLBRPEPFILDNQSLILNK 1133  
 DB 786 IISHELKGNINVEYCAVYCGFLAPSL-----KSKRVNTVYVKLRVQD 830  
 QY 1134 T-----NFTYPRVPEAFSPSGILEKPGTPIILKXKLIIPVAGNVANTVYVGER 1188  
 DB 831 TYIDCGTLQYREDPRRTGVR-----VESYDTELEVAIQ-----KENDNFMSKK 875  
 QY 1189 PCTVTV--SDVOLLCESPVLI-----GRHYMAVSGMEYS 1222  
 DB 876 DIBITLPHGNGQINCSFENITENODLITLCKIKIKTASTIANSKTVRVLGMLE-- 933  
 QY 1223 PGWYIAPDS-PLSLPAIVSIAVAGGLIIFIYAVLIAYYKRSRESDLTKRLQOMQDN 1281  
 DB 934 ---LYQGESVPSTWFLYLPV---LVYIVIAAGVIRHMSKE--LSKKQSG-QLELL 984  
 QY 1282 ESRVALECKEAFALQTDHETSLSDJGAG-IFPDYRYTYNVALEP--GIEHPVLRDL 1338  
 DB 985 ESELRKEIRIDGFALQMDKLDV---VDSFQTVFPLLYKHFALTFPPBSGGFTHTIEDW 1041  
 QY 1339 EYVGQYGERVEKGLKLEA--QLINNVKVFILSPRTLESQSPFMRDRGNVSLIMTVLQ 1396  
 DB 1042 ---HNSDANDKRESLTALDNLCKNSFLVTVVHTLEKQNGFVYKRCLEPASTLTALQ 1097  
 QY 1397 KLEAYADVLRQLADLIDKXLESKNHKKLLRRTESVAEKMLTNMFTFLYKFLKBCAGE 1456  
 DB 1098 KLVYLTSLLEVLTRDLMEQC--SNMOPKMLRRTESVVERELTNMNSVCLSGFLRETVGE 1155  
 QY 1457 PLPSLFCALIQOMEKGPIDAITGEARYSLSEDLILBQOQIDYKTLVYSCV---SPDNANSP 1513  
 DB 1156 PFYLLVTTLNQKINKGVDVITCKALYTLNEBMLNQVPEFSYALANVVEKIPENESAD 1215  
 QY 1514 ---EVPYKILNCDITIQVKEKILDAIFKQNVCSHRPRGADMDLEWQSGARMILQDEDI 1570

Db 1216 VCRNINNVNVDCTTIGQAKKIFQAFLSKNGSPYGLNIEIGLEOMGTROKELIDDS 1275  
 QY 1571 TTKIENDWKRLNTLAIYQVDPDGSVALVSKQVATNAVANNSTVSTASKENMIRYGS 1630  
 Db 1276 SVLEEDGITKNTIGHEISNGSTIKY-----FKCANFSD 1312  
 QY 1631 PDSLRSTPMTPTDLESQVMMVLVKNHEHGDQEGDRSK--MYSEIYLTRLLATKQTL 1688  
 Db 1313 VESVDHCHILIPDSR-----FQDVQCKH-----RKHKFKYKENVLTRLSTKAI 1361  
 QY 1689 QKAVDLEFETFTSTARGSLPLATKYMFDPLDEQDKGIDPHRYRTKNSCLPLRFW 1748  
 Db 1362 HSVLEKLFRTSISLPLN--SAPPAIKYFPFDQAQENKKTIDPVVHMKTNISLPLRFW 1419  
 QY 1749 VNMKNFQFVFDIHKNSITDACLVAQTFMDCSTSEHRLGKSPSKLLYAKDIPSYK 1808  
 Db 1420 VNLKNGFQFVFDIKPHIDGCLSVIAQAFDAFSLTBQOLGKAPTKLLYAKDIPYK 1479  
 QY 1809 NMYERYTSDIGKPAISDQMAAYLAQSRMNMENYMSALSEIFSVGKYSBEILGPL 1868  
 Db 1480 EEVASYKALRDPPLSSSEMEEFLOESKHEHNEFEVALTEIYKTVYFDEILNKL 1539  
 QY 1869 DHD---DQCGKOKIAYKL 1883  
 Db 1540 EREGLGEAQKOLLHVKV 1557

## RESULT 3

US-09-459-066-2  
 ; Sequence 2, Application US/09459066  
 ; Patent No. 6187909

## GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie  
 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
 TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Janis C. Henry  
 STREET: 51 University St.  
 CITY: Seattle

STATE: WA  
 COUNTRY: US  
 ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS/Windows 95  
 SOFTWARE: Word for Windows 95, 7.0a  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/459,066  
 FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/958,598  
 FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Henry, Janis C

REGISTRATION NUMBER: 34,347  
 REFERENCE/DOCKET NUMBER: 2631

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)470-4189

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1568 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 13.5%; Score 1349; DB 3; Length 1568;  
 Best Local Similarity 24.8%; Pred. No. 9,6e-112;  
 Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;

QY 72 YKLSDLKVLVTHETGDEEDNPKCYPRIVQTCNEPLTT-----NNVKNKLLIDYK 123  
 Db 70 YSLHSLSLRYNDQAG-----NCTEPVSLAPAPRPGSSFSK-LLLPYR 113  
 QY 124 ENR-----LIACSLYOGICKLRLLEDLFYLGEPYKKEHYLSGV-----NESGVFVG 172  
 Db 114 EGAAGLGGILLTGWTFEDRACGEVRLGVL-----SRNGLRNGTEVASCHPQGSTAGV 165  
 QY 173 IYSYENLDKXLFIA-----TADGKEVFPRTISSPKLKN 208  
 Db 166 VTR-AGRNRMWLAAYAVYLPEPETSRCNPASDHDTALALDQTRGSLATQELRLK 224  
 QY 209 EADGMFAVYFHDPEV-ASMKIPSPDPTIIPDPDIYVYGFSGNPFYFLTQEPVSP 267  
 Db 225 LCEGAGSLHFVDAFLMNGSIYFP-----YPPVNTSG-----AATGWSMARIA 268  
 QY 268 GSTTKEQVYTSKLVALCKEDTAFNSYVEVPIGERSGVE-YRLQAVLSAGAVLGRTL 326  
 Db 269 QST-----EVLFGQ--QASLDCHGHPDGRLLSSLYEA----- 302  
 QY 327 GVHPDDLLFTYFS--KQQRKMSLDSALCIFLQINDRIKERLOSCYRGSGLDLA 384  
 Db 303 -----LDVWAGVFSAAAGEQGERSSPTTALCLPRMSEIQRAKR-----VS 344  
 QY 385 W-LKVKXDIPCSSALLTIDNFCGLDMNAELGVSDMVGIPVFTEDRDMTVLAIVYKNH 443  
 Db 345 WDKPTAESHCXG-----DQF-----ERVPIASSTLIHSDLSVYGVTVNMR 387  
 QY 444 SLAFVGTSGKLLKIRIVDPRGNALQYETQV-----DPGYLRDMAFSKD 490  
 Db 388 TVLFLGTGGLLKYL-----GENLTSNCPREVIIEIKEPVFXKLVPDEY-----K 435  
 QY 491 HCOLYMSRDLTRPVESCGOYOSCGECGSGPHCGWCVLHNTCTRKESCEKSEPR 550  
 Db 436 NIYIYLTACKVRRIRVANCNKHSCECLTATPHCGWCHSLORCTFQGGC----- 487  
 QY 551 FASEKQCVRLTVHPNNISVSQVNVLLVETVNPBELSAGVNCFTFEDLSEMDGLVGNQI 610  
 Db 488 -----VHSENL-----NMLDISG----- 502  
 QY 611 CCYSPAAKVEPRIITENDHHVYOLKSKETGTFASTSVFVNGSVNSCL-SCVESP 669  
 Db 503 -----AKKCPKI-----QIRBSKRTIVTWGSP-----SPRHSCKVKNVDS 542  
 QY 670 YRCHWCIRYHCTHDPKTCFQEGRVKLPEDCPQLRVYDKILVEVYIKPITLAKKLPQ 729  
 Db 543 -----RELQ-----QKXQ 551  
 QY 730 POSGGRGECILNIQSEORVPLAFNSSSYOCONTSSXYEGMEINMLPEVLTVMR--G 787  
 Db 552 PNR-----TCICSI-----PIRAYKDVSVVNWMPFSG-----NMLSD 585  
 QY 788 HFNINDPACNKVHLKCGAMRBSGCLCKADPDACGCGCPGQCTLRQCHPAQESQMLE 847  
 Db 586 RNFNTN-----CSLKE-CPACVET-----GCWCKSARAC----- 615  
 QY 848 LSGAKSCTNPRITELIIVTGEREGTKVIRGENLGLHFEFDIASHYKAVAGECSPLVDG 907  
 Db 616 -----IHFTFA-----CDP-----S 625  
 QY 908 YTPAQIVCEM-----GEAKPSQHAGVEVCVAVCPREFPABASSQLYFWMTLTLSDLP 961  
 Db 626 DYERNOEQPVAVEKTSGGGRPKERK-----NRTQALQVYF-----IKSIEP 669  
 QY 962 SRGPMGGTQVYITGTNLAGSNV-VWFFGKQPC-----LFRHRSBSYIVCNTSSDEV 1014  
 Db 670 QKVTSLGKSNVAVTGANFTRASNITMLKGTSDCKDQVIGVSHVINDTHMKFSLPSGRK- 728  
 QY 1015 LEMK-VSVQVDPAAKHQDLVFGYVEDPRTIVRIEPMKSVSGNTIYAWGTHLDLQNPQI 1073  
 Db 729 -EKMDKVICQFDGNCSSVGSLSYIALPFGCSLIPATYIWSGQNTIMGRGKRVIDN--L 785

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QY 1074 RAKGGEKHINICEVINATEMTQAPALALGPDHGDILTERPEEFILINDVOSLLINK 1133
DB 786 IISHEIKGININSEYCAATYCGSLASL-----KSKKVTNTVLRVOD 830
QY 1134 T-----NFTYYPNVEAFGPGSILKPGTPIILKGKLIIPVAGNVKLVYLVGK 1188
DB 831 TYLDCGTLQVREDBRFTGYR---VESEVDTLEVKIQ-----KENDNENISK 875
QY 1189 PCVTV---SDVOLLCESEPLI-----GRHKMARVGGMEYS 1222
DB 876 DITTLFHSGNGQLNSFENITNODLTTLCKIKGKASTANSKKVRVYKLGLE-- 933
QY 1223 PGWYIAPDS-PLSLPAIVSIAVAGLLIIFVAVLIARKRSRSDTLKRLQOMQML 1281
DB 934 ---LYVQESVPSFTWYFLIYLPV---LVIVIFAAVGVTRHKSKE--LSRKOSQ-QLELD 984
QY 1282 ESRVALDECKAFALQTDIHELSDLDGAG-IFELDYRTYMKVLP--GIEDHPEVLRLD 1338
DB 985 ESELREKIRGDFALQMDKLDV---VDSFTVFFLDYKHPALTFPBGSGFTHTEDM 1041
QY 1339 EVPSYRQERYEKIKLPA--QLINNVKFLSFIRLESQSFSGMRDGNVAGIIMTVLOS 1396
DB 1042 ---HNRDANDKNESLALDALCNKSEFLVTVIHTLEKQNFVSVDRLFASFLITLALOT 1097
QY 1397 KLEVATVYLQALADLDKXLESKNPKLLRRTESAEMKLTNWFTELLYKLEKAGE 1456
DB 1098 KLVYLTILEVLTDLMEQC--SNMQPKMLRRRESVEKLTINMSVCLSGFLRETVSE 1155
QY 1457 PLFSLPAIKQOMKGPIDAITGEARYLSSEDKLIRQOIDYKTLVLSGV---SPDNANSP 1513
DB 1156 PFVILVTLINQINKGVVDVITCKALYTLNEDWLMQVPEFSTVALNVPEKIPENESAD 1215
QY 1514 ---EVYKILNCDTITTOYKEKILDAIKRNPVCSHRPKAAMDLEMROGSGARMILODEDI 1570
DB 1216 VCRNISVNVLDCTITGAKKIKIQAFLSKGSPGLQNLNIGLEQGTQKELLDIDS 1275
QY 1571 TTKTENMKRLNTLAHYQVDPDSYVALSVKQVTAYNANVSIVRTSASKYENMIRYTG 1630
DB 1276 SVILEDGTTKANTGHEISNGSTIKV-----FKLIANTSD 1312
QY 1631 PDLRSRTPMITPDLESQVKKMLVKQHEGDKGDRGSK--WSEIYITRLIATKGL 1688
DB 1313 VEYSDDHCHILIPDSEA---FQVQGRH-----RGRKRFVKVMYITKLSTVAL 1361
QY 1689 QKPVDDLPEITFSTAHRSALPLAIKMPFLDEQADKGIHPVYHTWZSNCLPLRFW 1748
DB 1362 HSAVEKIFRSIWSLPH--SRAPFAIKTFPDLQAEKKITDPAVHIKINSPLRFW 1419
QY 1749 VMINKPOFVFDIHKNSITDACLSTVAQTFMDSCTSEHRLGKDSPNKLIYADIPSXK 1808
DB 1420 VNILKNPOFVFDDIKTPIHIDCLSTVIAQAFMDAFSLTEOQIGKEAFNKLILYADIPYK 1479
QY 1809 NMVEYIYDIDGKPAISQDMNAYIABESRMNENFMTSALSEISFVGVYSEIIGPL 1868
DB 1480 EEVKSYAIAIDLPLSSSEMEEFITQESKQENEFNEVALTELIIKYIVYPIELINKL 1539
QY 1869 DHD---DQCGKQCLAYKL 1863
DB 1540 EREGLLEBAQKOLLHVXV 1557

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RESULT 4
US-09-459-065-2
; Sequence 2, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Sorligs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.

```

```

CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,065
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-459-065-2
Query Match 13.5%; Score 1349; DB 4; Length 1568;
Best Local Similarity 24.8%; Pred. No. 9,6e-112;
Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;
QY 72 YLSSDLKVLVTHGEPEDBNPKYPRPIVQTCNEPLTT-----NNVKNMLIDYK 123
DB 70 YSLHSLSRLVYRDQG-----NCTEVSALAPARPPSSSK-LLEPYR 113
QY 124 ENR-----LIACSLVYQICKLRLEDLFKLGEFYHKKHYLSGV---NESGVFQV 172
DB 114 EBAAGLGGLLLGWFFDAGACVRLGNL-----SRNSLRNGTEVYVSGHPQSGTAGV 165
QY 173 IVSYNLDKLFIA-----TANDGREYFPTISSRLTQNS 208
DB 166 VYR-AGRNRRWYLAAYTVIPEPETAQRCPNPAASHDTALAKDTGRLATQELGLK 224
QY 209 EADGMPAYVFHDEFV-ASMIKIPSDFTIIPDFDIYVYVYSGSNFYFTLQPEMVSPP 267
DB 225 LCGAGSLHFVAFVAFMNSIYFP-----YYPNYTSG---AATGPMARIA 268
QY 268 GSTTKEQVYTSKLVRLCKEDITAFNSYVEVPICGSGVY-YLLQAAVLSKGAVALGRLT 326
DB 269 QST-----EVLFGQ--QASLDGCGHDPGRRLLSSTLVEA----- 302
QY 327 GVHPDDLLFTVES--KQQRKMKSLDEBALCIFILKQINDRIKXRLQSVRGEGTDLDA 384
DB 303 -----LDVAVGVFSAAGSGGRRSFTTALCLFMSIQAARAK-----VS 344
QY 385 W-LKVDIPCSSALLTIDNFGCLDMNAPLVSDMVRGIPVTEBRDRTSYIAYVYK 443
DB 345 WDFKTAESHCKEG-----DQF-----ERVQPIASSTLTHSDLTSYGVTVNMR 387
QY 444 SLAFVGTSGKUKKLRVDPGRNALQYETQVYV-----DPQVLRDVAFSKD 490
DB 388 TVFLDTGSGQLKVL-----GENLTNCPVYIYEIKERTPVFYKLVDPVPV-----K 435
QY 491 HEQLYMSRQLTRPVESCGOYQSCGCLGSGDPHCGCVIANTTRKERGERSKERR 550
DB 436 NIYIYLTAGKVRIRIVANCNKHKSCSECTITADPCGCHSLQRTFGDC----- 487
QY 551 FASEMQCRLVTHPNNISVSQYNVLLVLETVNPELSAGVACTFEDLSMDGLVVGNOI 610

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Db 468 -----VSENLE-----NMLDISG-----502  
 QY 611 QCVSPAKEYRITTEGNDHVVOLQKSKETGTFASTFVYNGSVANSCL-SCVESP 669  
 Db 503 -----AKCPKI-----QIRSKKETTVMVGSF-----SPRISKGVANVDS 542  
 QY 670 YRCHWCKRYHCTHDPKTCGFBGCRVYLPEDCPOLARVNDKIYVAVIPILIKAKNLPQ 729  
 Db 543 -----RELJC-----QNSQ 551  
 QY 730 POSGQREYECTLINOSEORVPALRFNSSSVQOANTSYSEMEINNLVELTVVWN--G 787  
 Db 552 FNR-----TCTCSI-----PTRATYKDVSVVNVFSPG-----WNLSD 585  
 QY 788 HFNIDNPAONKHYLYKGAMRESGCLKADPDPACQCGPQCTLRHCHPAQBSQMLE 847  
 Db 586 RNFETN-----CSSLKE-CPACVET-----GCAMCKSARRC-----615  
 QY 848 LSGAKSKCTNPRITEIIPVTGPRGCTKVTIRGBNLGLBPRDIASHVKVAVGECSPLYDG 907  
 Db 616 -----IHFFTA-----CPB--S 625  
 QY 908 YIPAEQIVCEM-----GEAKPSQAHGPEVEIYVAVCHPZEMARSOLXYFMTLISDLKP 961  
 Db 626 DYERNOEQCPVAVEKTSGGGRPKENKG-----NETNALQVFF-----IKSIB 669  
 QY 962 SRGPNSSGTQVYITGTMLNAGSNV-VYMFGRKOP-----LFHRRSPYIVCNTTSSDEV 1014  
 Db 670 QKSTLGRSNVITVGTANFTASNTIMLKSTCDKQVIOVSHVLDTHKFKSLPSRK- 728  
 QY 1015 LEMK-VSVQVDRAKIHQDLVQYVEDPTVIRIBEMSVISGNTPIVWOTHLDLONPDI 1073  
 Db 729 -EMKDVCCIQFPGCNCSSVGSLSIALPHCSLIPATTWISGCGNTIMMGANDVDIN--L 785  
 QY 1074 RAKGQKHEINICEVLNATENTCOAPALALGPHQSDLTERPEEFILDNVQSLLINK 1133  
 Db 786 IISHLKNINIVSEYCATYCGFLAPSL-----KSSKRTVTVVKLRVOD 830  
 QY 1134 T-----NETYPNVFEAFPGSGILELKPGTPIILKKNLIPVAGNXYLVTVYNGK 1188  
 Db 831 TYLDGCTIQYREDRFTGYR-----VESEVTELEVKIQ-----KENDNFRISK 875  
 QY 1189 PCTVTV-----SDVQLCCSPMLI-----GRHVMARVGMEXS 1222  
 Db 876 DIEITLFGENGQINCSEFENTRNOUJTLICIKIKIKITASTIANSKYRVGLGMLB-- 933  
 QY 1223 FGMVYIAPDS--PLSLPAIVSIAVAGLLIFIVAVILAVYKRSRSDLTILKLOMOMXL 1281  
 Db 934 ---LYBOESVPSWYFLIVLPV---LVIYITPAVGVTRHKSKE--LSRKOSQ-QLELL 984  
 QY 1282 ESRVALBEKAPFABLQTDIHELTSDDLQAG-IPFLDYRYTMRVLPF--GIEDHPVLRDL 1338  
 Db 985 ESELRKEIRDFGFAELQMDKLDV---VDSFGTVFPLDYKHFALRTFPESGGFHTFTEEM 1041  
 QY 1339 EYPGYRQVRVKGKLFPA--QLINNKVFLSFRITESQSFEMRGRVAVASLIMTVLOS 1396  
 Db 1042 ---HNRANDKXESIRLADLICKNSFLVYVHTLEKONFESVDRCLFASFTIALQF 1097  
 QY 1337 KLEAVTDLKOLADLIDKRLNESKNHFKLLRRTESVAEMLTNMTFTLLYFLKEQGE 1456  
 Db 1098 KLVLTSLLEVLTRDLMEQC--SNMOPKMLRRTESVVEKLITNMVSVCLSGFLRTVGE 1155  
 QY 1457 PLFSIFCAIKQOMKSPIDATIGARYSLESDKLIROQIDYKTLVISCY---SPDNANP 1513  
 Db 1156 PFYLVLTTLNKKIKKPGVDVITCALYTLNEDMLWQVPEFSVALNVFEKIPREBSAD 1215  
 QY 1514 ---EYVYKILNCDITTOYKELIDAIKRNPCGSHRPADMDLEMQSGAGAMILODEI 1570  
 Db 1216 VCRNITSVAVLDDDTIGAKEXIFQAFLSKNGSPGQLMEIGLELQMGROKELLDIOS 1275  
 QY 1571 TTLEKENDKRLNTLAHVQVDPGSSVVALSVKQVYANVANSVTSRTSASKYEMIRYGS 1630  
 Db 1276 SVILEDGITKNTIGHYISNGSTIKV-----FKKIANFTSD 1312

QY 1631 PDLRSRTMTIPDLESQYKMHLYKNHEGQKGDGSK--WYSEIYLRLLATKQTL 1688  
 Db 1313 VEYSDHCHLILPDSA-----FQDVQGRKH-----RGKHFKYKEVYLRLLSTKVAI 1361  
 QY 1689 QKRVDDLFEITFSTARHGSALPLAKYMEPFLDEQADGHGHDHPVRRTKNSCLPLRFW 1748  
 Db 1362 HSYLEKLFBSIMSLPN--SRAPFALIKTFPDLDAQAEKKLITDPDVHIMKTNSLPLRFW 1419  
 QY 1749 VNMKNPQFVFDIHKNSITDACTSVAAQTENDSCSTSEHRLKXGKSPSKLLYANDIBGX 1808  
 Db 1420 VNLKNPQFVFDIKTTPHIDGCLSVIAQAFMDAFSLTEQOLGKAPYKTLIYARDIPYK 1479  
 QY 1809 NWYERYSDIGKMPAISQDDNMAVYLAQSRPMMEFNTMSLSEIFSVYKSEIIGPL 1868  
 Db 1480 EYVASYKAIKRIIDPLSSSEMEFLLQSKKHENFNEVALLTEYKIVIKYIPBEILNK 1539  
 QY 1869 DHD---DQCGKQKAYKL 1883  
 Db 1540 EREGRLEAKOKOLLHVKV 1557  
 RESULT 5  
 US-09-345-473E-24  
 ; Sequence 24, Application US/09345473E  
 ; Patent No. 6558903  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hodge, Martin  
 ; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/183781  
 ; CURRENT APPLICATION NUMBER: US/09/345, 473E  
 ; CURRENT FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ. ID NOS: 62  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 1404  
 ; TYPE: PRN  
 ; ORGANISM: Gallus gallus  
 US-09-345-473E-24  
 Query Match 5.4%; Score 538.5; DB 4; Length 1404;  
 Best Local Similarity 20.3%; Pred. No. 1.4e-38;  
 Matches 349; Conservative 223; Mismatches 548; Indels 599; Gaps 78;  
 QY 10 CLSHLLNMGSGSTLLTR-----OPAPLSQKRSFVFF-----RGPBAGFNLVDE 58  
 Db 5 CIVCLILL---APSLQAGAMQCRIRIPBSSTRNSVPTLPSLDAGSPVQ--NIAVFP 58  
 QY 59 RGHYILGAVNRILYKLSDLKVLVTHETGPDEDNKCYPRPIVQTCNPEPLTTNNVAKML 118  
 Db 59 DPTVFAVARNRLVDPFLRLRSVLVTPGTGSAB-CEICHLCPAAVADAPGEDVDNLL 117  
 QY 119 LIDYKERNLIAGSLVQIGICKLRLB-----DLRF--LGEYHKKHYLSGVN 164  
 Db 118 LIDPVPFWLYSCGTARGLCYLHQLDVRSSEVTLASTCTLSAANSVNCPPDVASPLG 177  
 QY 165 EGSQSVGVIVSNDLKKLFIATAVDK--PEYFP-TISSKRLTKNSADQMFAYVRHDE 221  
 Db 178 STAVIVA-----DRYASGYLSGVSSVAAVARSRSVAKRL--KTRRG-FADPRF-- 227  
 QY 222 FVAMIKIFSDFITIIPDFD---IYVYGGSSGNFVYFLTLPQPMWSPGSTKEOVYT 277  
 Db 228 -----SLTVLPHYQDVPIHYVHASFQDGHVLLVTVQPEF-----PSSST---FH 269  
 QY 278 SKVRLCKSDTLAFNSVVEVPIGC-----ERSGVE-----YRLQAAVYSKAGAV 321  
 Db 270 TRIVRSABEPELRKRRREIVLDCRYESKRRRRRAEETBRDVAVYVLLQAAHARPGAR 329  
 QY 322 LGRTLGHPPDDLLFTVSGQKRRYKSLDBSALCITFILKQINDRINKERLOSCTYRGECTL 381  
 Db 330 LARDLIDGTEVTVLFGAFESHPESRARQOHNSAVCAFPLRLINQAIRGMDKC----- 382  
 QY 382 DLWMLVKKOIPSSALLTIDDNFCGLDMNAPLGVGDMWRGIPVFTEDRMTSVIAYVYK 441

```

Db 383 -----CG-----TGTQTLKXGLAFQPGQ-----YC 403
QY 442 NNSLAFVGTSGKJIKRIKVDGPRGNALQYETVQVDBGPVLKDMASKDHQELIYSEKQ 501
Db 404 PHS-----VNLAPVNTISCMD-----Q 421
QY 502 LTRVAVSCGQYQSGECLSGDPHCGWCLANTCTRKCEKCEKRRFASGKQCVL 561
Db 422 PTLVPAAS-----H-----KV 432
QY 562 TVHNNNISVSGYANVLLETNNVPELSAGVNCFFEDLSEMDGLVGNQLOCTSPAKAYP 621
Db 433 DLFNGRLSGTLTISIPTVLQNV-----TVNHLGTAGQKRVL-----468
QY 622 RIITENGDDHVVQLOLSKSKETGMTFASTSFVFNCSVHNSCLSVESPYRCHMKCYRHVC 681
Db 469 GMLVQSSSYVAL-----TNF-----485
QY 682 THDKTSGFQGRVYKLPEDCPQLLRVDKILVVEVILKPTLTKAKMLPQPSGQRYECL 741
Db 486 -----SLGEPGLVQATGLQSHS--LL 505
QY 742 NIGSEORVPALRFNSSVOCNTSYSYEGMEINNLPELTVVNGHFNIDNPAQKVL 801
Db 506 FAAGTK-----VMRVNVVGPGR-----HFS-----526
QY 802 YKCGAMRESCGLCLKADPDPAKCGMCGPQCTTRQCHPAQESOMLELSGAKSKCTNPRIT 861
Db 527 -----TCRCILRARFMWCGMC--GNG--CTRHHBC--AGBWQ-----DSCP--PVLT 567
QY 862 EIPVGTGREGGTKYITIRGENLGLERF--DIASH-----VKAGVCSPLVD--G 907
Db 568 DFHRSAPLRQGTQVTL-----CGMTFHSPPDPTAHSLPQPYVAVAGHSCVTLDESSES 623
QY 908 YIF-----AQIYCEMGKAPKPSQAGFEICVAVCRPEMA-----SSQL--YIF 951
Db 624 YRPAPTRRKDPYVVLVCLVEPGEPAVAGPADVNVNTESACTSFVQGSSTLSGF 683
QY 952 MTLTSLDKSRGMSGGTQVTTIGTINLAGSNVVMFGKOPCLFRRSPS-----YIVCN 1007
Db 684 VEPHISTHPSFGQGGSTLMSLYGTHLSAGSSMRWTINSECLDQ--PSSGDGIRCT 742
QY 1008 TTSSDEVLEMVSVQVRAKIHQDLVQYVEDPTIYRIEPMWIVGNTPIAVWGHDL 1067
Db 743 APAATSLGAPVALMIDGEEFLAPLPEYRPDSVILVPCSY--GGSSTLTLIGTHLDS 800
QY 1068 IONQIPIRAK--HGKEHINICEVLANTE--MTCOPALALAPDHQSDLTRPEEFGILDN 1124
Db 801 VYRAKIQOGGGGGKTEATCEGQSPNMLCRSPAPI-----EIKVQNLSTLVDG 854
QY 1125 VQSLILANKINFTYYPNVPEARPGSG--ILEKPGCTIILKGNLPPVAGGVKLVNTYV 1183
Db 855 AADRMLF--RLRYFPQPMFSPGQGERYQLKGNELKVNQGLDSVAG--CENITM 908
QY 1184 LVGKEPCTVTVSDVOLLCESPNLI-----GHHKMARVQGWESYPGWYIAPDSPSLPAI 1239
Db 909 TVGGRDCHPNVLKNEVTCRVPBDVLTAPAGVQICVNGDCQALGV--LPASSLDMMA-- 965
QY 1240 VSIYVAGG--LLIIFIVAVLIANK--RKR-----ESDILTKRLQMDML 1281
Db 966 -SLALGTGVTFVLCVAVLRLRRMRKRGLNELLVHPRIEHPITIQ--PVVDYR 1022
QY 1282 ESSRYALBEKEAFALQTDIHETSLDLAG--IPFL-----DYR-----1318
Db 1023 EVQV-LPVAASPGIARPHAHFASGADAGGSVPULRTSCCLDLPELLEBKDIL 1081
QY 1319 -----TYMKRYL-----FGIDHVLVDL-----EYGYKREKV--1348
Db 1082 IPEBRLLTHRSRVIGRGHFGSVYHGYMDPLLQNLCAVKSILHRTDLEVEBEREGIL 1141
QY 1349 -----EKGKLPADLIINNKVLLSFIRTLF-----1373

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Db 1142 MKSFHHQVLSLGLVCLPRHGLPLVVLPMYRAGDILRHFIAGQERSPTVELLIGFGLQVAL 1201
QY 1374 -----SQRSPMD-----RNVASLIMTVQSKLEFAVATVL--KQLLADLIDKRLSKNPK 1424
Db 1202 GMEYLQKFKFHHDLAARNCMDETLTVKADPGLARDFGKEYV-----SIRQHRHAK 1255
QY 1425 ILLR--RTESVAKMLTN-----W--FTLLYKPLKXGAGPLPSLFCALKQOMKGPIDAI 1477
Db 1256 LPVKMMALIESILOKFTTKSDVMSFGVLMWELLTRGA-----SPYEVDPYDM--1303
QY 1478 TGEARYSLSEDKILROQIDYKL--VLSVSPDNANSP 1513
Db 1304 ---ARYLLRGRRLPQPPDPLVGVMLSCMAPTPBERP 1339

RESULT 6
US-08-556-422A-4
; Sequence 4, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIORIS, Vaessliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DPN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 607
; TYPE: PRN
; ORGANISM: Mus musculus
US-08-556-422A-4

Query Match 3.1%; Score 308; DB 4; Length 607;
Best Local Similarity 21.5%; Pred. No. 2e-18;
Matches 144; Conservative 110; Mismatches 257; Indels 160; Gaps 29;

QY 36 KORSFTFRGEPAPGHNHLYVDBERTGYLGAVNRHYKLSPTKLYVTHE-----TGDE 90
Db 1 EBLIKKFEHENSNTALLISODGKTLVYGAREALFALNSHLSFLPGHYVELLMSADA 60
QY 91 DNRKCYPRIVQTCN---EPLTTNNVNMKLLIDYKENLLIAG--SLYQIGCKLLRLD 145
Db 61 DRK-----QQCSKQKDPKRDCCNYIKILL--PLNSHLLTTCGTAFFSPICAYIHAS 111
QY 146 LFLGEPYHKKHLYLGSVSGSVFGLVYSNLD-----DLGFTATA--VYGRPEY 195
Db 112 -FLIAQ-----DEAGNVI-----LEDGKHCFPDNFKSITALYVDG--EL 148
QY 196 F-----PTISSRLTKNSEDGFAVVFDEFYASMIKIPSDFTIIPDFDIY 244
Db 149 YTGVSFGQNDPAISRQSSRPKTESLNLQDPAFAVASPSPESLSPIGDDKLYF 208
QY 245 VYGSSGNFVYFLLTPENWSPGSTTKEQVYTSKLVLCCKEDTA-----FNSYEV 296
Db 209 FFSGTGGEFF-----ENTIVSRVAKCKDBEGGERVLQGRMTSFLKA 252
QY 297 PIGGER--SGVEYRLQAAVLSKAGAVLGRTLGVHDD--DLTFVSKGQKRRKKSUD 351
Db 253 QLLCSRDDEFPENVIQDYF-----TLNPNQDRKTLSIGVFSQWR--GTE 300
QY 352 ESALCIPILKQINDRIKERLOS CYRGEGLDLAM--LKVDICSSALLTIDNFCGLDMN 410
Db 301 GSALCVYTM--ND--VQKAFDGLYKVNRELTQMTTEHTQVTPPGACITSAERKIN 356
QY 411 APGVSD-----MRGIPVTEBRDKTYSIAN--VKNHSLAVGTS 452
Db 357 SSIQLEPRVNLFLKDFLMDQVRSRLILQPRARQVAVARVPGHSTYDVLFGTD 416

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453 GKLKIRYDGRGNALQYETVQVVDPGFVLDMAFSKDHBQLYIMSEBOLTRVPEVSCQ 512  
417 GRHKAVTLASRVHII---EELQIPQOQPVQNNLLBDSHGLVLAASHGVGVANGL 474  
513 YQSGCEGLSGSDPHCGM---CVLHNT-----CTRKECERSKERERRA 552  
475 YPTGDCDILARDPYCAMTGSACRLASLYQDPLASRPOTDIEASVKECKXSSYKARPL 534  
553 SEMKQCVRLVHPNNISVQYVLLVLET---YNNPELSAGVNCCTFEEDLSEMDGLVGN 608  
535 VPKRCKQVQIQPTVNTLACPLLSNLTATRLMWNHNPVAVASGRV--LPDGLLLVGS 592  
609 Q-----IQCY 614  
593 QQGLGVFQCMS 603

## RESULT 7

US-09-077-940A-4  
Sequence 4, Application US/09077940A  
Patent No. 6576441  
GENERAL INFORMATION:  
APPLICANT: KIMURA, Toru et al.  
TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME  
FILE REFERENCE: 0020-4426P  
CURRENT APPLICATION NUMBER: US/09/077, 940A  
CURRENT FILING DATE: 1998-06-05  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 888  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-077-940A-4

Query Match 2.6%; Score 263; DB 4; Length 888;  
Best Local Similarity 23.7%; Pred. No. 4.8e-14;  
Matches 144; Conservative 90; Mismatches 208; Indels 192; Gaps 34;

11 LLSHLNVMGMSSTLLTRQAPALSOQKQSFVTF-----RGEPAEGFHLVVD-- 57  
13 LLLLLLLLG-GAHGLFEDPEPLSVARPDYLNHYFVVGSGPGRLTPEAGADLNIQRYL 71  
58 --ERTGHYLGAVNRIYKL-----SSDLKV--LVTHETGSDENPKCYPRIVQTCNRP 107  
72 RVNRT--LFIQDRMLRVELLEPPTSTELRYOKRLTRSNPSINCRKKGQEGECR-- 127  
108 LTTNNVNMKMLIDYKENRLIAGCS-LYQGI CKLLRLLEDL FKLGE-----PYHKKEH 158  
128 ---NFYKVLRLD--ESTLFCGSAFNPCANYSIDLQPVGDNISGARCPYDPK-H 180  
159 YLSGNEGSGVFGIVS-----YSNDDKLFITAVDGKREVEFPITSSKLTKNSE 209  
181 ANVALFSQMLFTATVIDFLAIDAVIYRSLGDR-----FLIKRYK----- 220  
210 ADGMPAVYHDEFAVSMIKIPSDFTIIPFDIYVYVYFGSSGNFVYFLTLQPEMVSPPGS 269  
221 ---HD---SKWFKEP-----YFVAVEMGSHVYFFREIEM--EF 252  
270 TTKEOVYTSKVLCKEDTA-----FNSYVEVPIGERSG---VEYRLIQAAVLSK 317  
253 NYLEKVVSVRAVCCKNDVGSFVLEKQWTSFLKARLNSVPGDSHFYFNVLQAV---- 308  
318 AGAVLGRITLVHPDDDLFTYFSKGQRKKSJDESALCTFIKQINDRIKERLQSCVYG 377  
309 TGVV--SLGRP---VLAIFS---TPSNSIFGSAVCAFDLQVAAVEGR---FRE 354  
378 EGTLDLWALKYKD--IP-----SSALLITIDNFCGIDMNA---PLGSDMWGRGIPVT 426  
355 QKSPESITVTPBEDQVRRPRGCCA-----PGQVYASASALDDDLNPFKTHPLMD 406  
427 ED-----RDMTSTVIAVY---YKNSLAVGTSGKLKIRY-----D 461

407 EAVPSLGHAFWILRLIMRHLTRVAVDVGAGWGNQTVFLGSEAGTVLKFLVRENASTS 466  
462 GPRGNALQYETVQVVDP-----GPVLRDMAFSKDHBQLYIMSEBOLTRVPEVSC 510  
467 GTSGLSYFLFEFTYTPDKCRPGGGEFGQRLSLSELDASGGLMAFPKCVRYVPVARC 526  
511 GQYQSC-GECLSGSDPHCGM---CVLHNTCT 538  
527 QQYSGCKMKCIGSQDPCGMADPGSCIFLSPGTR 560

## RESULT 8

US-09-077-940A-2  
Sequence 2, Application US/09077940A  
Patent No. 6576441  
GENERAL INFORMATION:  
APPLICANT: KIMURA, Toru et al.  
TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME  
FILE REFERENCE: 0020-4426P  
CURRENT APPLICATION NUMBER: US/09/077, 940A  
CURRENT FILING DATE: 1998-06-05  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 2  
LENGTH: 887  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-077-940A-2

Query Match 2.4%; Score 244.5; DB 4; Length 887;  
Best Local Similarity 22.2%; Pred. No. 2.3e-12;  
Matches 141; Conservative 86; Mismatches 206; Indels 203; Gaps 34;

8 WT-----CLSHLNMVGMGSSSTLLTRQAPALSOQKQSFVTF-----RGEPAE 49  
2 WTRAPRPPRALLFLILLRLRVTHGLFPEDEPLSVARPDYLNHYFVVGSGPGRLTPEAE 61  
50 GPNHLYVD-----ERTGHYLGAVNRIYKL-----SSDLKV--LVTHETGSDENPKCY 96  
62 GAEDLNIQRYLAVNRT--LFIQDRMLYQVELEPSTSTELRYOKRLTRSNPSD----- 113  
97 PRPIVQTC---NEPLTTNNVNMKMLIDYKENRLIAGCS-LYQGI CKLLRLLEDL FKLGE 151  
114 ---IDCRKKGQEGECNPFYKVLRLD--ESTLFCGSAFNPCANYSMDTLQLLGD 167  
152 -----PYHKKEHLSGNEGSGVFGIVS-----YSNDDKLFITAVDGKRE 194  
168 NISGMARCPYDPK-HANVALFSDGMLFTATVIDFLAIDAVIYRSLGDR----- 214  
195 YPPTISSRKLTKNSEADGFAVYHDEFAVSMIKIPSDFTIIPFDIYVYVYFGSSGNFV 254  
215 --FLIKRYK-----HD---SKWFKEP-----YFVAVEMGSHV 242  
255 YPPTIDPEMVSPPGSTTKEQVYTSKVLCKEDTA-----FNSYVEVPIGERSG- 304  
243 YFFREIEM---EFNYLEKVVSVRAVCCKNDVGSFVLEKQWTSFLKARLNSVPGD 298  
305 --VEYRLIQAAVLSKAGAVLGRITLVHPDDDLFTYFSKGQRKKSJDESALCTFIKQ 362  
299 SHEFYNVLQAV---TGVV--SLGRP---VLAIFS---TPSNSIFGSAVCAFDVNO 344  
363 INDRIKERLQSCVRCGGTLDLWALKYKD--IP-----SSALLITIDNFCGIDMNAPIGV 415  
345 VAAVFSR---FREKSPESITVTPBEDQVRRPRGCCA-----PGQVYASASAL 392  
416 SD-----MYRGIP-----YTEDRDMTSTVIAVY---YKNSLAVGTSGS 452  
393 PDEILNFVKTFLPMDAVVSLGHSFWITVTLIRHQLTRVAVDVGAGWGNQTVFLGSEV 452  
453 GKLKKT-----RVDPGRGNALQYETVQVVDP-----GPVLRDMAFSKDHBQL 494  
453 GYVVKFLVPMASVSGTTPSIFLEBEFTYRDRGRSSSAGWKQRLSLSELDASAGL 512



QY 495 YIMSERQLTRVYVESCQGYOSC-GECLSGDPHCGM 529  
DB 513 IAAFPRCVAVFVARCOLYSGCMKNCIGSDPYCGM 548

## RESULT 9

US-08-121-713D-62  
Sequence 62, Application US/08121713D  
Patent No. 5639856  
GENERAL INFORMATION:  
APPLICANT: Goodman, Corey S.  
APPLICANT: Kolodkin, Alex L.  
APPLICANT: Matthes, David  
APPLICANT: Bentley, David R.  
APPLICANT: O'Connor, Timothy  
TITLE OF INVENTION: The Semaphorin Gene Family  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,713D  
FILING DATE: 13-SEP-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B94-002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415) 343-4342  
TEXT:  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 724 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-713D-62

Query Match 2.3%; Score 227; DB 1; Length 724;

Best local similarity 20.4%; Pred. No. 5,9e-11;

Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

QY 53 HLVDERTGHIYGAUVRIRYKLSDDLKAVYTHETGPDENPKCYPRIVQTCNEPLTTN 112  
DB 72 HAMEEDRT-LYIGANDRVPRV-NQNTSSSNCNDALN-----LEPRDDVASCV 119  
QY 113 NVAKMLLDYKENRLIACGSLYOGICKLRLLEDLFGLGEPYHKEHY-----LSGVNBSG 167  
DB 120 SKGKSOIFDCK-NHVRVIGMDQG-----DRLVCGTNAHPKDYVIYANLTHLRSE 171  
QY 168 SVRGVAVS-----YSNLDDLFIATAV---DGKPEYFPITSSRKLKNSADQMFAYVH 219  
DB 172 YVIGVGIGIKACYDPIDN---STAIYENGNPGLFGLYSTNAEFTKAD---TVIR 224  
QY 220 DEFVAMIKLPSDTFTIPDFDI-----YVYGFSSGNFVFLIQP---EMVSPGSGTT 271  
DB 225 TDLYNISAKLEKFKKTKLKYSKMLDKPFGVSPDIGEVYVFFRETAVEYN---C 279  
QY 272 KEQVYTSKAVRLCKEDPA-----FNSVVEVPICGRSG---VEYRLQAAVYSKAGA 320  
DB 280 GKAVY-SRIARVCKQDVGGKMLAHMWATYLRKRLNCSISGEPPFFNEIQSYV----- 332

QY 321 VLGRITGVHPDDDLTFVFSKQKRMKSLDSEALCIFIILKQI-----NDRIKERLQSCYR 376  
DB 333 -----QLPDSKSRFRATFT-----TSTNGLISAVCSFHINELQAAFNKFKRQSSS--- 379  
QY 377 GEGTLDLAWLKVXD--IPCSALLTIDNFCGLDMNAPLGVSDMVGIP----- 423  
DB 380 -----NSAWLFLVINSRVBEPRPGTCVNDT-----SNLPDTVINFIKSHPLMDKAVNHEHN 429  
QY 424 -----VFTE-----DRDMTSLVAVYKNNSLAVGKSGGLKKIRVDGPRGNAL-QY 470  
DB 430 NPVYKREDLVFTGLVVDKIR---IDLNOEYIVYVGNLNGRIYKIYQYIRNGESLSKL 485  
QY 471 ETVOVVDPGFVLDRDMAFSKDHEQLYTMSEROLTRVPEVSCG-OYSGCGECLSGDPHCGM 529  
DB 486 LDIFEVAPNEALQVMEISQTRKSLYIGDHRIRQIDLAMCNRRYDNCFRCV--RDYPCGM 543  
QY 530 CVLHNTCTRKER-----CERSKEPRRFSKMKQCYRLVHPNNNISVSQYNYL 576  
DB 544 DKRANTCRPYELDLDDVANETSIDCDSVLRKKIIVYTGQSVHLGCF----- 591  
QY 577 LVLETYVVPPLSAGVANCCTFEDLSMDGLVYGNQICQYSPAKKEVPRITTEMGDHHVVOIQ 636  
DB 592 -----VXIFEVLRKNEQVYTHHSKDKGRY---EIR-YSPTR-----YIETTERGLVAVS 636  
QY 637 LKSKETGNTFASFSFVFNCSVHNSCLSCVSPYRCHWKYR-----HYCTHDPKYSFQ 691  
DB 637 VNEADGR-----YDCHLGSSLL-----CSYNTVDAHRCPTPENKSDYQ 676  
QY 692 E 692  
DB 677 K 677

## RESULT 10

US-08-835-268-62  
Sequence 62, Application US/08835268  
Patent No. 5807826  
GENERAL INFORMATION:  
APPLICANT: Goodman, Corey S.  
APPLICANT: Kolodkin, Alex L.  
APPLICANT: Matthes, David  
APPLICANT: Bentley, David R.  
APPLICANT: O'Connor, Timothy  
TITLE OF INVENTION: The Semaphorin Gene Family  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/835,268  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,713  
FILING DATE: 13-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B94-002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415) 343-4342  
TEXT:  
INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 724 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-835-268-62

Query Match 2.3%; Score 227; DB 1; Length 724;  
 Best Local Similarity 20.4%; Pred. No. 5.9e-11;  
 Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

53 HLVDERTGHIYLGAVNRIRYKLSOLKLVTHETGPDENPKCYPRIVGTCNEPLTTN 112  
 72 HMEEDRT-LYVGANDRVFRV-NLQNISSNCNRDAIN-----LEPTDDVAVSCV 119  
 113 NVNKMILLIDYKRNRLIACGLYQICLRLLEDLFKLGEPYHKKEHY-----LSGVNESC 167  
 120 SKGSKQIFDCK-NHVRVIGSMDOG-----DRLVYCGTNAHPKDYIYANLTHLPRE 171  
 168 SVFGVIVS-----YSNLDKLFATAV--DGKPEYPTISSRKLTNKSADGMFAVVFH 219  
 172 YVIGVGLGIAKCPYDPLDN-----STAIYVENGNPGGLPGIYSGTNAEFTYAD--TVIFR 224  
 220 DEFVASMIRIPSDTFTIIPDFI-----YVYGFSSGNVYFLLTLP--EMVSPGSTT 271  
 225 TDLVNTSAKRLEKFKRLTKYDSKMLDKPNFVGSFDIGEVYFFPRETAVEYIN-----C 279  
 272 KEQVYTSKIVRLCKEDTA-----FNSYVEVPICGERSG--VEYRLQAAYLSKAGA 320  
 280 GRAVY-SRIARVCKKDVGGKRLAHNMATYLAALNCSISGEFPFYNEIQSVY----- 332  
 321 VLGRTLGVHPDDLLFTVFSKQGRKMSLDESALCTFILKQI--NDRKELQSCYR 376  
 333 -----QLPSDKSRFFATFT--TSTNGLIGSAVCSFHINEIQAFNGKFEQSSS-- 379  
 377 GEGTLDLAWLKVKD--IPCSGALLTIDNFCGLDMNAPLGVDVNRGIP----- 423  
 380 -----NSAMLPVLSRVEPRPGTCVNDT--SNLPDTYANLFRSHPLMDKAVNHEHN 429  
 424 -----VFTE--DRDRTSVIAYYKNSLAFFVGTSGSKLTKKIRVDGPRGNAL-QY 470  
 430 NPVYKRDVFTKLVVDKIR--IDLINQEIYIYVYVGNLBRITKIYQVYNGSLSKL 485  
 471 ETVOVVDPGCVLDMAPSKDHEQLYMSERQLTRVVESSG-QYQSGCGCLSGPRHGM 529  
 486 LDIFEVAENPAIQMEISQTRKSLYIGTDHRIKQIDLAMCNRRYDCFRCV--RDYCGM 543  
 530 CVLHNTCTRKER-----CERSKEPRRFASSEMOCVRLTVHFNNTSVSQYVNL 576  
 544 DKEANCTRPYELDLQDVANETSDICDSVLKKKIYVYTGSHLQCF----- 591  
 577 LVLETYVNPPLSAGVNCTEFEDLSMDGLVGNQIQCSPAKAEVPRITTEGNDHAYQIC 636  
 592 -----VKIPRYLKNQYTWYHNSKDKGRY--EIR-YSPTR-----YIETTERGLVAVS 636  
 637 LKSEKTEMTFASISFVFNYSVNSCLSCVESPYRCHWCYR--HYCTHDPKTCSPQ 691  
 637 VNEADGGR-----YDCHLGGSLL-----CSYNTVNAHAKTTPKNSNDYQ 676  
 692 E 692  
 677 K 677

RESULT 11  
 US-09-060-692-62  
 Sequence 62, Application US/09060692  
 Patent No. 5935865  
 GENERAL INFORMATION:  
 APPLICANT: Goodman, Corey S.  
 APPLICANT: Kolodkin, Alex L.  
 APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy  
 TITLE OF INVENTION: The Semaphorin Gene Family  
 NUMBER OF SEQUENCES: 100  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 268 Bush Street, Suite 3200  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/060,692  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/121,713  
 FILING DATE: 13-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: B94-002-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)343-4341  
 TELEFAX: (415) 343-4342  
 TELEX:  
 INFORMATION FOR SEQ. ID NO: 62:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 724 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-060-692-62

Query Match 2.3%; Score 227; DB 2; Length 724;  
 Best Local Similarity 20.4%; Pred. No. 5.9e-11;  
 Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

53 HLVDERTGHIYLGAVNRIRYKLSOLKLVTHETGPDENPKCYPRIVGTCNEPLTTN 112  
 72 HMEEDRT-LYVGANDRVFRV-NLQNISSNCNRDAIN-----LEPTDDVAVSCV 119  
 113 NVNKMILLIDYKRNRLIACGLYQICLRLLEDLFKLGEPYHKKEHY-----LSGVNESC 167  
 120 SKGSKQIFDCK-NHVRVIGSMDOG-----DRLVYCGTNAHPKDYIYANLTHLPRE 171  
 168 SVFGVIVS-----YSNLDKLFATAV--DGKPEYPTISSRKLTNKSADGMFAVVFH 219  
 172 YVIGVGLGIAKCPYDPLDN-----STAIYVENGNPGGLPGIYSGTNAEFTYAD--TVIFR 224  
 220 DEFVASMIRIPSDTFTIIPDFI-----YVYGFSSGNVYFLLTLP--EMVSPGSTT 271  
 225 TDLVNTSAKRLEKFKRLTKYDSKMLDKPNFVGSFDIGEVYFFPRETAVEYIN-----C 279  
 272 KEQVYTSKIVRLCKEDTA-----FNSYVEVPICGERSG--VEYRLQAAYLSKAGA 320  
 280 GRAVY-SRIARVCKKDVGGKRLAHNMATYLAALNCSISGEFPFYNEIQSVY----- 332  
 321 VLGRTLGVHPDDLLFTVFSKQGRKMSLDESALCTFILKQI--NDRKELQSCYR 376  
 333 -----QLPSDKSRFFATFT--TSTNGLIGSAVCSFHINEIQAFNGKFEQSSS-- 379  
 377 GEGTLDLAWLKVKD--IPCSGALLTIDNFCGLDMNAPLGVDVNRGIP----- 423  
 380 -----NSAMLPVLSRVEPRPGTCVNDT--SNLPDTYANLFRSHPLMDKAVNHEHN 429  
 424 -----VFTE--DRDRTSVIAYYKNSLAFFVGTSGSKLTKKIRVDGPRGNAL-QY 470  
 430 NPVYKRDVFTKLVVDKIR--IDLINQEIYIYVYVGNLBRITKIYQVYNGSLSKL 485



MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,610  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/835,268  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B94-002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
TELEX:  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 724 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-060-610-62

Query Match 2.3%; Score 227; DB 4; Length 724;  
Best Local Similarity 20.4%; Pred. No. 5.9e-11;  
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

QY 53 HLVVDERTGHIYGA VNRIRYKLSDELKVLVTHETGPEDEPKCYPRIVOTCNEPLTTN 112  
DB 72 HNNEDRDT-LYVGAMDRVFRV-NLQNISSNCRDAIN-----LEPTDDVAVSCV 119  
QY 113 NVNKKLLIDYKENRLIAGSLYOGICLRLLEDLFKLGEPYHKKEHY-----LSGVNBSG 167  
DB 120 SKGSKQIFDCK-NHVRVIGSMDOG-----DRLVYCGTNAHPKDYIYANLTHLPBSE 171  
QY 168 SVFQVIVS-----YSNLDDKLFATAV---DGKPEYPTTISRKLTKNSEADGMFAYVPH 219  
DB 172 YVIGVGLGIAKCPYDPLDN---STAIYVENGNPGGLGIVSGTNAFTKAD---TVIFR 224  
QY 220 DEFVASMIKIPSDFTITIPDPDI-----YVYVGSNGFVYELTLPQ---EMVSPGSGTT 271  
DB 225 TDLVNTSAKRLYEYKFKTLKYSKWLDPKPNFVGSFDIGEYVFFFRRTAVEYIN-----C 279  
QY 272 KEQVYTSKVLRLCKEDTA-----FNSYVEVPICGERSG---VEYRLQAYLSKAGA 320  
DB 280 GKAVY-SRLARVCKKDVGSKNLLAHNMATYIKARLNGSISGEFPYFNEIQSVY----- 332  
QY 331 VLGRITLGVHPDDLLFTVFSKQKRKMSIDESALCIFILKQI---NDRIKERLOSQYR 376  
DB 333 -----QLPDSKSNRFAFT---TSTNGLIGSAVCSFHINEIQAFNGKFKQSSS--- 379  
QY 377 GEGTIDLAWLKVKD--IPCSSALLTIDNFGGLMNAPLGYSMDVRIP----- 423  
DB 380 -----NSAMLPVILNSRVEPRPGTCVNDT---SNLPDTVLANFRSHPLMDKAVNHEIN 429  
QY 424 -----VFTE---DSDRMTSVLAAYVYKNSHSLAFVQTSKGLKKTIVDGPGRNAL-QY 470  
DB 430 NPVYVKRLVFTKLVNDKIR---IDLNGEYIYVYGTNIGRIYKIVQYRBNGESLSKL 485  
QY 471 ETVOYVDDGVPVLRDMAFSKDHEQLYINSEBQLTVPVPSGCG-QYQSGGECGSGSDPRHGM 529  
DB 486 LDIFEVAPNEAIQVWEISQTRKSLYITGDHRIKQIDLAMCNRRDNCFRCV--RDPYCGM 543  
QY 530 CVLHNTCTRKER-----CEKSKERRPASEMKQCVRLTHPNNISVSQYVNL 576  
DB 544 DKEATCTCRPYHEDLLQDVANETSJCDSSVLKKKIIVLYGQSVHLGCF----- 591  
QY 577 LVLETVNPEISAGVNCFTFEDISEMDGLVGNQIQCSPPAAKEVPRITITENGHHVYQLO 636

DB 592 -----VKIPEVLKNEQVTHYHNSKDKGRY---EIR-YSPK-----YIETTERGLVVS 636  
QY 637 LKSKETGMPASTSFFVYVYNSVHNSCLSVESPYRCWKYR-----HCTHDPKYCSFO 691  
DB 637 VNEDADGR-----YDCHLGGSLIL-----CSYNTVDAHRCCTPBNKSNQYDQ 676  
QY 692 E 692  
DB 677 K 677

## RESULT 14

PCT-US94-10151A-62  
Sequence 62, Application PC/TUS9410151A

GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10151A

FILING DATE: 13-SEP-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299 FHT UR

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 724 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-10151A-62

Query Match 2.3%; Score 227; DB 5; Length 724;  
Best Local Similarity 20.4%; Pred. No. 5.9e-11;  
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

QY 53 HLVVDERTGHIYGA VNRIRYKLSDELKVLVTHETGPEDEPKCYPRIVOTCNEPLTTN 112  
DB 72 HNNEDRDT-LYVGAMDRVFRV-NLQNISSNCRDAIN-----LEPTDDVAVSCV 119  
QY 113 NVNKKLLIDYKENRLIAGSLYOGICLRLLEDLFKLGEPYHKKEHY-----LSGVNBSG 167  
DB 120 SKGSKQIFDCK-NHVRVIGSMDOG-----DRLVYCGTNAHPKDYIYANLTHLPBSE 171  
QY 168 SVFQVIVS-----YSNLDDKLFATAV---DGKPEYPTTISRKLTKNSEADGMFAYVPH 219  
DB 172 YVIGVGLGIAKCPYDPLDN---STAIYVENGNPGGLGIVSGTNAFTKAD---TVIFR 224  
QY 220 DEFVASMIKIPSDFTITIPDPDI-----YVYVGSNGFVYELTLPQ---EMVSPGSGTT 271  
DB 225 TDLVNTSAKRLYEYKFKTLKYSKWLDPKPNFVGSFDIGEYVFFFRRTAVEYIN-----C 279  
QY 272 KEQVYTSKVLRLCKEDTA-----FNSYVEVPICGERSG---VEYRLQAYLSKAGA 320  
DB 280 GKAVY-SRLARVCKKDVGSKNLLAHNMATYIKARLNGSISGEFPYFNEIQSVY----- 332

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QY 321 VLGRLLGVHDDDLLFTVPSKQGRKKKSLDESALCIFILKQI-----NDRIKERLOSQCYR 376
DB 333 -----QLPBDKSRFFATFT-----TSNGLIGSAVCSFHINELOAANFGKFKQSSS----- 379
QY 377 GEGTLDLAWLKVKD--IPCSSALLITIDNFCGLDMNAPLGVSDMVRGIP----- 423
DB 380 -----NSAMLPVINSRVSEPRPGTCVNDT-----SNLPDVLVLFIRSHPLMDKAVNHEHN 429
QY 424 -----VETE---DQDRMTSVIAYVYKNSHSLAFVGTSGKLKIRVDGPRGNAL-QY 470
DB 430 NPVYVKDVLFTKLVNDKIR-----IDLNGEYIVYVYVGNLGRILYKYVYRNGESLSKL 485
QY 471 ETVOGVDPGVLKDMAFSKDHEQLYINSEKOLTRVPVESCQ-QYOSCGECLSGSDPHCGM 529
DB 486 LDIFEVAFNEAIQVMEISQTRKSLIYIGTDHRKIQIDLAMCNRRYDNCFCRCV-RDYPCCGM 543
QY 530 CVLANTCTRKER-----CERSKEPRRFAEMKQCVRLTFVHPNNISVSQVNYL 576
DB 544 DKEANTCPYELDLQDVANETSDICDSSVLKKIIVTYGQSVHLGCF----- 591
QY 577 LVLETYVPELSAGVNCITFEDLSEMDGLVVGNOIQCYSPAKAEVPRITTEGSHVYQLO 636
DB 592 -----VKIPEVLKNEQVLTWYHNSKDKGRY---EIR-YSPTR-----YIETTERGLVYVS 636
QY 637 LKSKETGNTFASSTFVFNCSVHNSCLSCVSESPYRCHMCKYR-----HVCETHDPKTCSPQ 691
DB 637 VNEADGGR-----YDCHLGSL-----CSYINITVDARCTCPNKANDYQ 676
QY 692 E 692
DB 677 K 677

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RESULT 15  
US-08-121-713D-58  
; Sequence 58, Application US/08121713D  
; Patent No. 5639856  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matches, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,713D  
; FILING DATE: 13-SEP-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 730 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-58
Query Match 2.1%; Score 207; DB 1; Length 730;
Best Local Similarity 18.9%; Pred. No. 3,8e-09;
Matches 111; Conservative 107; Mismatches 219; Indels 150; Gaps 27;
QY 43 FRGEPAEGFNHLYDERTGHIYLAQVNIYKLS-SDL-----KVLVHETGPPEDNPKCY 96
DB 41 FLGNESHHDHFKLEKHNLSLVGARNTVNIISRLDLEFTEQRIEMWSSGABRE-LCY 98
QY 97 -PPRIYQCNPEPLTTNNVNMGLLDYKENTLIAGC-SLYOGICKLALTEPDLFKIGSEYH 154
DB 99 LKGSSEDDCQ-----NIRVLAKID--DKVLTICGINAYEPDLRHYALKD-----GDYV 146
QY 155 KKE-----HYLSGVNCSGVFVIVS-YSNLDDKLFTATAVDGKPEYFPITSS 201
DB 147 EKEVEYGRGLCPDPDHNSTAIYSEGLYSATVADPFGSDPLIYRG-----PLRTE 196
QY 202 RCLTKNSADGKFAVHFHDEFVASMIXIPSDPTITIPFDIYVYGFSSGNFVFLTIQP 261
DB 197 RSDLKQLANPENVNTEYNDPL-----FFPFRTAVEYI---NCGKAIY----- 237
QY 262 EWVSPGSGTKEQVYTSKLVELCKEDTA-----FNSYVEVPICERSGVYERLLQAA 313
DB 238 -----SVAARVCKHDKGPHQGGDRWTSFLKSRINCSPVG-DYPFYENE 280
QY 314 YLSKAGAVLGRTLGVHPDDDLLFTVPSKQGRKKKSLDESALCIFILQINDRIKERLOS 373
DB 281 IOSTSDIIEGNYG--QVEKLIYGVFT---TPVNSIGSVAVCASMSK---ILSEFDG 330
QY 374 CYRGEGLDLAWLKVKDI-----PCSSALLITIDNFCGLDMNAPLGVSDMVRGIPVF 425
DB 331 PKKEGTNMSNMLAVPSLKVPEPRPGQCVNDSRLPD---VSVNFVKSHTIMDAVPAF 386
QY 426 TEDRDMTSVIAVYV-----KNSLAFVGTSGSKLKT-----RVD 461
DB 387 FTRPILIRISLQYRFTKLAVDQVTPDGKAVDYLFTIGDQKVKALNSAFDSSDTPD 446
QY 462 GPRGNALQYETVOVDPGVLEDM---AFSKDHEQLYINSEKOLTRVPVESCQ-QYOSC 516
DB 447 -----SVVIEELQVLPFGVPAKLVVAMDGDGSLVYVSDDEILAIKLRGSGSKITNC 501
QY 517 GECLSGDPHCGMCVLHNTCTRKERCERSKEPRR-----ASEMKQC 558
DB 502 RECVSLODPYCAMDNVELKCTAVGSPDWSAGRRFIONISLGEHRAC 548

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Search completed: February 18, 2004, 16:42:28  
Job time : 37 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 16:40:25, Search time 51 Seconds

(without alignments)  
7784.094 Million cell updates/sec

Title: US-09-964-956-13

Perfect score: 1 MKAMPNMTCLSHLMVGM.....QKLAYKEQVITLMSLDNKK 1896

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA:  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*  
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13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1814	18.2	344	12 US-10-108-260A-3245	Sequence 3245, App
2	1609.5	16.1	1806	12 US-10-369-493-5622	Sequence 5622, App
3	1351.5	13.5	552	10 US-09-909-320-170	Sequence 170, App
4	1351.5	13.5	552	10 US-09-909-0888-170	Sequence 170, App
5	1351.5	13.5	552	10 US-09-905-291A-170	Sequence 170, App
6	1351.5	13.5	552	10 US-09-902-853-170	Sequence 170, App
7	1351.5	13.5	552	10 US-09-907-824-170	Sequence 170, App
8	1351.5	13.5	552	10 US-09-907-841-170	Sequence 170, App
9	1351.5	13.5	552	10 US-09-904-011-170	Sequence 170, App
10	1351.5	13.5	552	10 US-09-906-742-170	Sequence 170, App
11	1351.5	13.5	552	10 US-09-906-838-170	Sequence 170, App
12	1351.5	13.5	552	10 US-09-907-613-170	Sequence 170, App
13	1351.5	13.5	552	10 US-09-907-842-170	Sequence 170, App
14	1351.5	13.5	552	10 US-09-904-859-170	Sequence 170, App
15	1351.5	13.5	552	11 US-09-909-204-170	Sequence 170, App

16	1351.5	13.5	552	11 US-09-904-820-170	Sequence 170, App
17	1351.5	13.5	552	11 US-09-904-786-170	Sequence 170, App
18	1351.5	13.5	552	11 US-09-906-646-170	Sequence 170, App
19	1351.5	13.5	552	11 US-09-906-700-170	Sequence 170, App
20	1351.5	13.5	552	11 US-09-903-786-170	Sequence 170, App
21	1351.5	13.5	552	11 US-09-902-903-170	Sequence 170, App
22	1351.5	13.5	552	11 US-09-903-749A-170	Sequence 170, App
23	1351.5	13.5	552	11 US-09-904-119-170	Sequence 170, App
24	1351.5	13.5	552	11 US-09-904-956-170	Sequence 170, App
25	1351.5	13.5	552	11 US-09-902-734-170	Sequence 170, App
26	1351.5	13.5	552	11 US-09-907-794-170	Sequence 170, App
27	1351.5	13.5	552	11 US-09-903-943-170	Sequence 170, App
28	1351.5	13.5	552	11 US-09-904-462-170	Sequence 170, App
29	1351.5	13.5	552	11 US-09-907-925-170	Sequence 170, App
30	1351.5	13.5	552	11 US-09-902-692-170	Sequence 170, App
31	1351.5	13.5	552	11 US-09-903-520-170	Sequence 170, App
32	1351.5	13.5	552	11 US-09-905-056-170	Sequence 170, App
33	1351.5	13.5	552	11 US-09-909-064-170	Sequence 170, App
34	1351.5	13.5	552	11 US-09-904-553-170	Sequence 170, App
35	1351.5	13.5	552	11 US-09-905-381-170	Sequence 170, App
36	1351.5	13.5	552	11 US-09-907-575-170	Sequence 170, App
37	1351.5	13.5	552	11 US-09-905-075-170	Sequence 170, App
38	1351.5	13.5	552	11 US-09-902-759-170	Sequence 170, App
39	1351.5	13.5	552	11 US-09-902-634-170	Sequence 170, App
40	1351.5	13.5	552	11 US-09-902-713-170	Sequence 170, App
41	1351.5	13.5	552	11 US-09-907-979-170	Sequence 170, App
42	1351.5	13.5	552	11 US-09-902-615-170	Sequence 170, App
43	1351.5	13.5	552	11 US-09-903-925-170	Sequence 170, App
44	1351.5	13.5	552	11 US-09-906-760A-170	Sequence 170, App
45	1351.5	13.5	552	11 US-09-906-760A-170	Sequence 170, App

## ALIGNMENTS

RESULT 1  
US-10-108-260A-3245  
; Sequence 3245, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3245  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-108-260A-3245

Query Match 18.2%; Score 1814; DB 12; Length 344;  
Best Local Similarity 100.0%; Pred. No. 5e-157;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1551	MDLEWRQSGAMILLQDEDDITIKINDMKRLNTLAHYQVDPQSVVALVSKQVATYANVNN	1610
DB	1	MDLEWRQSGAMILLQDEDDITIKINDMKRLNTLAHYQVDPQSVVALVSKQVATYANVNN	60
QY	1611	STVSRTSASKYENMIRYGSPPSLSRPTMTPTDLESQVQWHLVKNHEHGDQKEGDRGS	1670
DB	61	STVSRTSASKYENMIRYGSPPSLSRPTMTPTDLESQVQWHLVKNHEHGDQKEGDRGS	120
QY	1671	KVASEIYLRLATATGTLQKFPDDLFEITFAHGSALPLAIKXMPFLDQADKXGH	1730
DB	121	KVASEIYLRLATATGTLQKFPDDLFEITFAHGSALPLAIKXMPFLDQADKXGH	180
QY	1731	DPVHRTKSNCLPLRFVWMIKNPQFVFDIKNSITDACLSSVAQTFMDCSTSEHRIG	1790
DB	181	DPVHRTKSNCLPLRFVWMIKNPQFVFDIKNSITDACLSSVAQTFMDCSTSEHRIG	240

QY 1791 KDSPEKLLYKADISYKWERRYSDIGKPAISDQDMNAYLAQSGRMHNEENTMSAL 1650  
DB 241 KDSPEKLLYKADISYKWERRYSDIGKPAISDQDMNAYLAQSGRMHNEENTMSAL 300  
QY 1851 SEIFSYGKYSEELGPLDHDQCGKQKLAAYLEQVITLMSIDS 1894  
DB 301 SEIFSYGKYSEELGPLDHDQCGKQKLAAYLEQVITLMSIDS 344

RESULT 2  
US-10-369-493-5622  
; Sequence 5622, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianteng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052) B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 5622  
; LENGTH: 1806  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-5622

Query Match 16.1%; Score 1609.5; DB 12; Length 1806;  
Best Local Similarity 26.4%; Pred. No. 7e-137;  
Matches 525; Conservative 346; Mismatches 773; Indels 341; Gaps 81;

QY 11 LLSHLLMVGMSSTLITROPAPISQKRSFVTFKSPAGFNMHVYDERTGHILYGANR 70  
DB 37 LISHFRA-----YTOPFETEGYQKLFHFSGH-----IDDFIVSRDQQTIVASLNR 85  
QY 71 IYKLSDDLKYLVTHER--GPEDNPKC-----YPPRIYQTCNEPLTTN 112  
DB 86 LTLISLTS-NEISIGHEVSLGVDSPWCSADGSKCLTVNQHVFIIIFRDNRPPT-- 142  
QY 113 NVNKMILLIDYKENLLIACGSLYQIGICKLRLEDLPKLGEPYHAKGHEYLGVNSESQV 172  
DB 143 DVRTKILQILPTNQLIQCGSVKLGSC-----STFNK--LSLITES-----T 182  
QY 173 IVASN-----LDDKLFIATAVDGKREY--FPTISSRKLTKNSEADGMP--A 215  
DB 183 IANAANSPDASTYKTIIDNRLIYAASATKSPRDPPPAVALNGLAVENAGDLEGA 242  
QY 216 YVDFEFAVMIKIPSDTFTIIDFDIYVYGSGNFYFLTLQPEMTSPPOSTTKEQV 275  
DB 243 AVFLRAAYKNAFK-----FLYTFHQHFVVA-----MYTPRESRLP-- 280  
QY 276 YTSGLVLLCKEDPAFNSVVEVIGCE-RSGVEYRLQAAVLSKAGAVLGGTGVHDDDL 334  
DB 281 MTRKLLIFCRNDITFBSYSEIELQCGEDNTNYPFLNAIIQSY-----DK 325  
QY 335 LFTVFSKQOKKMKLSDESAICIFILQINDRIKRIQSCYRSEGTDLAMLKVCIDPCS 394  
DB 326 LIASFST-----STSPKSIQVFSMOKVLTFFWYNDRCRSGDISIRLPHIG-RDTKC- 378  
QY 395 SALLTIDNFGGLDMNAPLIGSDMVRGIPVETED-RDRMTSVIAYVYKNSLAFVGTSG 453  
DB 379 KAHPLLEBDS-----ELGVGSGIEIVENSTKDIIMKVTSLNAV--DKALFAGTTIS 429  
QY 454 KLRKIRVDPGRNAL-QYETVQVVD--FGPYLRDMASFSDHOLYIMSERQLTRVVEGC 510  
DB 430 QIVFKWDEHNSNOLEBYGRKEVGDGRGSEVSKV--KFGDPIVQMPYGIILBELSTC 487

QY 511 GQYOSCGECLSGDHPHCGVLTNLTCTRKERCERSEKPPAFASEMKQC--VRLTHPNNT 568  
DB 488 SHHSCTECLVAVDPLCQWCHPTQSTTSARCT-----SPVTSQCGIVGDPIPSIV 539  
QY 569 SVSQNVVLVLETYNVPELSAGVNCFF-----DISEMDGLVGNQIOCYSPAKEVPI 623  
DB 540 SVNSSTPI-----SFNHLHPPEVGTTCRCQGTSTSSIAMWTTTGVSGPS-----BI 588  
QY 624 ITENDGHVVOQLKSKETGMTFASTSFVYVNCVSNCLSCVSPYRCHWKYRHVCTH 683  
DB 589 FTSPPNFEILLTSSINN--PISRNFTVYDCSGVGTSCMSSESNYNCAMSGJHKCSN 645  
QY 684 DPTCSFQBRGYVLPEDCPQLRVKILVVEV--IKPITLAKXNLPQOSQORGE--C 739  
DB 646 ---SC---GALEKSTAC--VKIQPRLPIAGSQOETVLEASNL--DTIDRREHFC 692  
QY 740 ILNIGSEORVPALRFNSSSVQCCNTSYSEGEIMNLLPELVVVA--NGHFNIDNPAQNK 798  
DB 693 KVN-----EVSIAKIASDSIRCKIQLTSLNTSAMVVPISLIRDSVIDIAN----- 742  
QY 799 VHLKCGAFRESCGLCKADPDACGCGPQCTTROCQPAESQMLSEKSKCTNP 858  
DB 743 VSLYCTNLASDCSCIALSPSLSCWCN--RQCSHECH--BSK-----ATAVCDP 790  
QY 859 RITEIIPVGRREGKTVIRGENLGLPEFDIASHKVAVGECSPVVDGYIPAEQIVCEM 918  
DB 791 RIDPFTSPJIRGGITIKIYNDLGMASVEDVAGKIVVAGSRGN--IVEHVNMIACQV 848  
QY 919 GEAKPSQAGFVEICVAVCRPEPMARSQIYYMTLLTSLDKSRGPMGSGIYVITGN 978  
DB 849 DKGVSS---GPIRISGARATVA--VAESSELYSFVRSITSFAYPLVGPISGRTITLYGON 904  
QY 979 LMGSNVYVWFGKQPCFHR-RSPSYVCTTSSDEV-LEMKYSVQVDFRAKIHQDLVFOY 1036  
DB 905 LSSGSQTSVVGMPCEIERVNSYVLTCLTPSGTRIGKARVAVVHDHQQLDQPEFY 964  
QY 1037 VEDEPTIVRIPEWSIYSGNPIAVWGLHLDLIGNPQIRAHGKHEINI-----CEVLA 1090  
DB 965 RSDPSISIFPMTSFKAIGRIYVYOGNSLTVQTAFLISSPTPEYIISDLAPCHLIN 1024  
QY 1091 ATEMTQCAPALALGPDQSLTERBEFGITLVNOSLILNTKTFYYNPPFEAFGPS 1150  
DB 1025 STLNTCMTPK-----LLETIRARVYVYVQPMQIYNPPLISPP--K 1062  
QY 1151 GILELKPGTPIILKGNLIPVAGNVL--NYTVLGEKPCCTVYSDV-QLICSEPNL 1206  
DB 1063 GVRVHQBQSLIEGHNL-----NLAEPNDFKIFIGNERCYVTLVDVROLVCSGP-- 1113  
QY 1207 IGRK-----VMAVYGMESVPGVNYIAPDSPSLSPALVSIIVAGGLII 1251  
DB 1114 VROPATDERGIPINGNPVLTIVGSLRHELGLEY--SDHALPRLSLILIG--LLL 1168  
QY 1252 FIVAVL-----IAYRKRESDELTLKRLQMDNLSSVVALECKEAPAELOTD--THELTS 1305  
DB 1169 FIVTLVTVGLVFRBRROEREKEYRKTQLQENIENNVRKECKQAFALQTNILSPKSA 1228  
QY 1306 DLDGAGLPFLDYRTYKAVLP--GIEDHPL--RDLVPGVRGRVEKGLFQALINNK 1362  
DB 1229 NSVNLGPELINFPHVENILMSDNNLTSAEPLATLPV-----LAQFALLSFK 1278  
QY 1363 VELSIFRLESQSFMSRDRGNVASHIMTVLQSKLEVAIDVLKOLLADLIDKLESKNH 1422  
DB 1279 GRIFTIVAAASDVISISTSEKMLASLISVLBNFSYCFEVVDLRAHARAVQNK-R 1337  
QY 1423 PXLIRKTESVAEKKLTWTFLLYKPLKEAGRPESLPALCAQOMKEGSDIATGPAR 1482  
DB 1338 AELFRNDSVVEKPFKMSWISCIYSHLTPQMS-YFLVYKALQYQIDKGVADVATGPAR 1396  
QY 1483 YLSDEKLIROQIDVKTIVLSVSPDNANSPEVVKILNCDTITQVEXKILDAIFKONVC 1542  
DB 1397 YVINAKILRESVDIKILIR-VIFEKCDSDIDLEVACDAICQVKOKVASAVYRETPY 1455  
QY 1543 SHRPADMDLEMRQSGARMILQD---EDITTKIENDMK---RLNLTAVYQVDDGSVV 1595

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Db 1456 SORPRITQELKCKPKRQDVLTDLVLEPIETLSCK-----KLPHYKLTADYGISDQCTL 1510
Qy 1596 ALVSKQVAVYANVANNSTVTSRTSASKYEMIRYTG--SPDSLRSRTPMITDLSGVGMW 1653
Db 1511 EKSPAVYI-----ABSYRSLDSCQSMSLDRSP-----IYSSKYH 1551
Qy 1654 LYKNEHGD---QKEGDRGS---RMSELYTLATKGTLLQKFEVDLFEITFSTAHNG 1706
Db 1553 LT-NSSSGMTPEKKSSNDNLPPKSIPEVYLTLLSKGTVEYVEDFLESVLYM--HD 1608
Qy 1707 SALPLAIKMFEDLEQADKHGIDPHYRRTMKNCCLPLRWVMINQPFVFDIHNSI 1766
Db 1609 SSYPILKFFFDILDRASVNGVB--NICQMKANGVLRWMAFVNPQLVDFVHSIS 1667
Qy 1767 TLACISVVAQTMDSCSTSEHRLGKDFSNKLTAKDIPSTYKMWERYSDIGKMPAISD 1826
Db 1668 MDANISTVAQTMDCFSSESVLGAHSPSSLLFPAKVARIPLSVDLFRKXNSPPLCW 1727
Qy 1827 QDMNAVLAEGSRMHNENFTMS---ALSEIFSYGKYSEIILGPDLDHDOCKOKLAKY 1882
Db 1728 DELRTELNVMA---NDVSTCKSSSLALSELISWVRNGIRISQLLSSNQGFCQRLPK 1783
Qy 1883 LEQVI 1887
Db 1784 LSQVL 1788

```

RESULT 3  
 US-09-909-320-170  
 Sequence 170 Application US/09909320  
 GENERAL INFORMATION:  
 APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Geber, Hanspeter  
 APPLICANT: Gerltsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tunas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/909,320  
 PRIOR FILING DATE: 2000-01-04  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08

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/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 170
/ LENGTH: 552
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-909-320-170

Query Match 13.8%; Score 1351.5; DB 10; Length 552;
Best Local Similarity 51.6%; Pred. No. 3,4e-114;
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

Qy 23 STLTROQAPLPSOKR-----SFTPRGEPAB- 49
Db 45 SRLIT--APPLSMEGRPMWRALVDSRSVYLLSVWVLAPPAACMPGFSTFHSNRM 102
Qy 50 GFNHLVVDERTGHIIYLGAVNRIRYKLSDDLKATVTHETGDEDEPKCYPPRIYQCKEPLT 109
Db 103 TFNHLVHQGTGAVYGAIRVYKLGMLTIQVARTGPEEDNKSRYPLIYQPCSEVLT 162
Qy 110 TTNVNVGMLIDKKEKRLIACGSLYQGICTLRLDLEFLKGEFYHKKHAYLSGVNCSGV 169
Db 163 LTNVNVKLLIIDSERKLLACGSLYQGVCKLRDLFLVRSKHKEHYLSVYKGTGM 222
Qy 170 FGVIVSYNSLDDKFLATAVDGKPEYFPTISRKLTNSBADOMFAVYHDEFVASMKI 229
Db 223 YGVIVRSBGEDGKFLGTAVDGKDYFPTLSRKLPREDSSAMLDYELHSDPVSLLIKI 282
Qy 230 PSCDFTIIPDFIVYVYVGFSSGNFYFLTLOPMVSPG---STYGEQYTSKLYLCKE 286
Db 283 PSDTLAVSHDFIYIYGFASGGFYFLTYQPE--TPREGVALNSAGDLYTSRIYRLCKD 340
Qy 287 DTFANSTYEVPIGCGNSGVETRYLLQAYLSKAGAVLGRTLGHPDDLLFTVFSKQCKRK 346
Db 341 DPKFHSYVSLPFGCTAGVETRYLLQAYLAKPDSIAQFNTSQDVLFAFSKQCKQY 400
Qy 347 MKSIDESALCTIFIKQINDRIKERLOSRYGEGTDLAMIKVYDIPCSALLITIDNFCG 406
Db 401 HHPRDSALCAPIRLAINIDIKRLOSQYGBENLEMLNLLKDVQCTGAPPIDNFCG 460
Qy 407 LDMNAPRGVSDMVRGLPVFTEDDQMTSVIAYYKXHSALAFGTSGSKLKKLRVDGPRN 466
Db 461 LDINQPLGSGTPEVGLTYTTSRDMTSVASYVYNGSVVFGTSGSKLKKVRV----- 514
Qy 467 ALQYE-----TVQVVDGPYLARMARSK--DHEQLYTMSRQ 501
Db 515 ---YEPKSNVAILHLSKESLISGSSYWMRFVYRLVYLGQR 552

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RESULT 4



```

US-09-909-0888-170
Sequence 170, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,658
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20344
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 170
LENGTH: 552
TYPE: PR1
ORGANISM: Homo sapiens

```

```

US-09-909-0888-170
Query Match 13.5%; Score 1351.5; DB 10; Length 552;
Best Local Similarity 51.6%; Pred. No. 3,4e-114;
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

QY 23 STILLROPAPLSQQR-----SPTTFGEPAE- 49
DB 45 SRIILT--AAPLSMBQROPWRALFEVDSRVVLSVWVLLAPPAAGMPQFETPSEKEDW 102
QY 50 GFNLVYDERGHIYLGAVNRITYKLSDDLKVLVTHETGPDDEDNPKCYPPRIYQTCNEPLT 109
DB 103 TFNHLTHGCGAVYVGAIRNVYLTGNLTITQVAKHKGPEEDNSRPPLIVQCSFVLT 162
QY 110 TTNNVTKLLIDYENRLLIACGSLYQGI CKLRLIEDLPKLGEPYHKKENHLYSGVNGGSV 169
DB 163 LTNVNVKLLIDYSENRLLIACGSLYQGCCKLRLIDDLFILEPBEKHENHLYSVNKGITM 222
QY 170 FGVIYSVSNLDDCKFIATAVDGKEFEPTTSSRLKLTNKSSEADGMFAVYFHDEFVASMIRI 229
DB 223 YGVIVRSBGECEGCKLFIQAVVDGCKDYPFTLSSRLKLPBPBSSAMLDYHSDFVSLIKI 282
QY 230 PSDFPTIIPDDIYVYVIGFSSGNVYFTLTLPKAVSPG--STTKQVYNSKLVRLCKE 286
DB 283 PSDTLALVSHDIFRIVYVGFAGGVYFLVQPE--TPEGVAINSAGDIFYSRLVRLCKD 340
QY 287 DTAFSYVEVYIGCGRSGVEYRLQAAAYLSKAGAVLGRITLVHPDDLLFTVFSKGQQRK 346
DB 341 DPKHASYSLPFGCTRAQVEVRLIQAAYLAPGDSLAQAFNITSDDVLFPAIFSKGQKQY 400
QY 347 MKSLDESALCIFLKQINDRKERLQSGSYRREGTLDLAWLKVRIQCSALLTIDDNFCG 406
DB 401 HRPDDDSALCFPIRAINLQIKERLQSGSYQSGNLTMLWLGKDVQCTKAPAPIDNFCG 460
QY 407 LDMAAPLVSVMVNGI PVFTEDRDRMTSVIAYVYKNHSLAEVGTGSKLTKLIRVDGPRGN 466
DB 461 LDINPLOGSPVPSBELTLTYTTSRDMTSSVASYVNGYGVVFGVTKSGKLTKKRV----- 514
QY 467 ALQYE----TVQVVDPPGVRLDMAFSK-DHEQLYIMERQ 501
DB 515 --YEFRCNAIHLISKESLLEGSYWMFNPTRQLTYFLEGR 552

RESULT 5
US-09-905-291A-170
/ Sequence 170, Application US/09905291A
/ Patent No. US2002160374A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillen, Kenneth, J.
/ APPLICANT: Kijavita, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumala, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.

```

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/905,291A  
;; CURRENT FILING DATE: 2001-07-12  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: 2000-02-22  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 170  
;; LENGTH: 552  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-905-291A-170  
Query Match 13.5%; Score 1351.5; DB 10; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3,4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;  
QY 23 STLTROPAPISQOR-----SVTTRGEPAR 49  
DB 45 SRLTL--AAPLSMQRPPWRALEVDRSVVLISVVWVLLAPPAAGMPQSTHSESRDD 102  
QY 50 GFNLVVDERTGHIYLAQVNRITYKLSDDLKVLVTHETGDEDDNPKCYPRIVOTCNBPLT 109  
DB 103 TFNHLTHGCGAYVVAIRNVYLTJTNLTIQVANKTGPEDDKSRPPLIVQPCSVLTI 162  
QY 110 TTNVNTKLLIDYENRLLIACGSLYOGICKLLLEDFKICEPHKKEHLISGVNSGV 169  
DB 163 LTNVNTKLLIDYENRLLIACGSLYOGICKLLRDLDFIIVEPBKKEHLISVNTKGTW 222  
QY 170 FGVVSYNLUDDKFIATVADGKPEYPTISSRKLTKNSADGFAVVFDEFVAAVYIKI 229  
DB 223 YGVIVRSBGEDGKFIQAVDGKODYFTLSRKLPRDPSSAALDYELHSDPVSSLIKI 282  
QY 230 PSDFTTIIIPDIIYVYVGFSSGNFVYPLTLOPEWVSSPG--STTQCVTTSKLVRLCKE 286  
DB 283 PSDTLAVSHPDIFITYVFAAGGFYFLVQPE--TREGVAIVSAGDLFTYSRIVRLCKD 340  
QY 287 DTAHSYVEVPIGCRSGVEYRLLQAAVLSKAGAVLGRSTLGVHDDDLFTVFSKQGRK 346  
DB 341 DPKHSYVLPFGCTRAQVEYRLQAAVLAAPGSLAQAFNITSQDDVLAIRFSKQGRK 400

QY 347 MKSIDESALCFILKQINDRIKERLOSQYRGEGLDLAMTKVYDIPCSSALLTIDNFCG 406  
DB 401 HHPDSDALCAFPFIRAINLQIKERLOSQYRGEGLDLAMTKVYDIPCSSALLTIDNFCG 460  
QY 407 LDNNAPLGVSDMWYGVIFVFEEDRDGMTSVIAYYKNSLAFVGTSGKLRIRYDGRGN 466  
DB 461 LDINQPIGGSTPVEGLTLTYTSRDRMTSVASYVNGYVVFVGTSKGLKKVRV----- 514  
QY 467 ALOYE-----TVQYVDPGPIVLRDAFSAK-DHEQYIMSEQ 501  
DB 515 --YEFRCNAIHLISKESLIEGSGYWMRFNIRQLFIQEGR 552  
RESULT 6  
US-09-902-853-170  
Sequence 170, Application US/09902853  
Publication No. US20020192659A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Deanoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Klagsan, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/902,853  
;; CURRENT FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: US/09/665,350  
;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02

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us-09-964-956-13.rapb

Page 6

PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 170  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-902-853-170

Query Match 13.5%; Score 1351.5; DB 10; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3.4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

23 STLTROPAPLSQKOR-----SEVTFGEPAE 49  
45 SRLLT--AAPLSMEQOPWPALEVDSRSVLLSVVWVLLAPPAGMPOFSTFHSENDW 102  
50 GFNHLVYDERTGHIYIGAVNRITYKLSDLKAVYTHETGPDDEPNKCYPRIVQTCNEPLT 109  
103 TFNHLTVHOGTGAVYGAIRNRYKLTGNLTQVAKHTGPEEDNKRYPPLIVQPCSEVLT 162  
110 TTNNVKKMLIIDYKENRLIACGSLYOGICKLRLBEDLFLKGEPRYKKEHYLSGVNESA 169  
163 LTNNVKKMLIIDYSENRLIACGSLYOGVCKLRLDLDLFLVPSKKEHYLSVANKTGT 222  
170 FGIVYSVNDLDFLTAIVDGPPEPPTISSKRLTKSEADGMFVYHDEPVASMTKI 229  
223 YGVIVSEGGDGLFTGTAVDGQDFPFLSSKRLPRDESSAMLYELHSPVSSLLKI 282  
230 PSTFTFIIPDFIYVYVFGSGNFVYFLTLQPEMVSPPG---STTRGEVYTSKLVRLCKE 286  
283 PSTLTALVSHFDLFIYVFGSGNFVYFLTVQPE--TPBGALVNSAGDLFYTSRIYVLC 340  
287 DTAFNSTVEVPIGCGSGVEYRLLOAAYISKAGAVYGRILGVHPDDLLFTVPSKQK 346  
341 DPKFHSVSLPFGCTRAGVRYRLLOAAYLAKPDSDSLAQAFNITSQDVFALFSGKQ 400  
347 MKSLDESAICIFILKQNDRIKERLSCYRGEGLDLIAWLKVDICSSALLTIDNFC 406  
401 HHPDDSAALCFIRAINLQIKERLSCYRGEGLDLIAWLKVDICSSALLTIDNFC 460  
407 LDNNAPLGVSDMYRGIPIVFTEDSDRMTSVIAYYKNSLAFVGTSGKGLKLRVYDPR 466  
461 LDINQPIGSGTPVEGLTLYTTSRDMTSVASVYVNGSVVFEVGTSGKGLKRVV----- 514  
467 ALOYE-----TVGVVDPGPVLRDMAFSK--DHEOLYIISERO 501  
515 ---YFRCNSAIHLISKESLBSGYMRFYRQLYFLGEOR 552

RESULT 7  
US-09-907-824-170  
Sequence 170; Application US/09907824  
Publication No. US20020197671A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Geo, Wei-Qiang  
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,824  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 170  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-907-824-170

Query Match 13.5%; Score 1351.5; DB 10; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3.4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

23 STLTROPAPLSQKOR-----SEVTFGEPAE 49  
45 SRLLT--AAPLSMEQOPWPALEVDSRSVLLSVVWVLLAPPAGMPOFSTFHSENDW 102  
50 GFNHLVYDERTGHIYIGAVNRITYKLSDLKAVYTHETGPDDEPNKCYPRIVQTCNEPLT 109

Db 103 TFMHLTVHOGTGAIVYGAIRNRYKLTGNLTIIQVAHKTGPEDNKSRYPLIYQPCSEVLT 162  
Qy 110 TTNVNNKMLIDYKENVRLIACGSIYOGICCKLRLEDLFLKGPYHKKHEHLSGVNBSGSV 169  
Db 163 LTNVNNKMLIIDYSENRLIACGSIYOGICCKLRLEDLFLIYVSHKHEHLSVNNKTGM 222  
Qy 170 FGVIVSYNLDKLFIAVAVDGKEPEYPTISSRKLTKNSPADGMFAVYHDEFAVSMITK 229  
Db 223 YGVIVRSEGEDEKLFITAVDGKODYPTLSSRKLPRDPSSAMLYELHSDVSSILIKI 282  
Qy 230 PSDFTIIPBDIYVYVGSFGNFFVLTLOPEVNSPPG---STTKBOVYTKVLCKE 286  
Db 283 PSDTALVSHFDIYITGVASGCFVYFLVQPE--TPGVAINSGADLFTTSIVLCKD 340  
Qy 287 DTAFNSYVEVPICERSGVEYRLIQAAVLSKAGAVLGRITGVHPDDLLFTVFSKQQRK 346  
Db 341 DPKFHSYVSLPFGCTFRAGVEYRLIQAAVLAAPGDSLAQAFNITSODDVLFAIFSKQQRK 400  
Qy 347 MKSLDEBALCIFILKQINDRIKEXLSCYRGEGLDIAWKVDDICSSALLTIDNPGC 406  
Db 401 HHPDDSLACAFPIRALNLOIKERLQCYGBGNLWMLGKOVCTKAPVPIIDNPGC 460  
Qy 407 LDMNAPLVSDMVRGIPFTEDRDGMTSVIAYVYKNSIAFVGTSGKLRKIRVDGPRGN 466  
Db 461 LDINQPLGSGTPVGLTYTTSRDRMTSVASYVNGYVVFVGTSGKLRKIRV----- 514  
Qy 467 ALQYE-----TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501  
Db 515 ---YEFRCNAIHLKSKESLLEGSYWMRFNYRQLYFLGEQR 552

RESULT 8  
US-09-907-841-170  
Sequence 170, Application US/09907841  
Publication No. US20020198366A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroli, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Maher, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907, 841  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143, 048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145, 698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146, 222

Qy 103 TFMHLTVHOGTGAIVYGAIRNRYKLTGNLTIIQVAHKTGPEDNKSRYPLIYQPCSEVLT 162  
Db 163 LTNVNNKMLIIDYSENRLIACGSIYOGICCKLRLEDLFLIYVSHKHEHLSVNNKTGM 222  
Qy 170 FGVIVSYNLDKLFIAVAVDGKEPEYPTISSRKLTKNSPADGMFAVYHDEFAVSMITK 229  
Db 223 YGVIVRSEGEDEKLFITAVDGKODYPTLSSRKLPRDPSSAMLYELHSDVSSILIKI 282  
Qy 230 PSDFTIIPBDIYVYVGSFGNFFVLTLOPEVNSPPG---STTKBOVYTKVLCKE 286  
Db 283 PSDTALVSHFDIYITGVASGCFVYFLVQPE--TPGVAINSGADLFTTSIVLCKD 340  
Qy 287 DTAFNSYVEVPICERSGVEYRLIQAAVLSKAGAVLGRITGVHPDDLLFTVFSKQQRK 346  
Db 341 DPKFHSYVSLPFGCTFRAGVEYRLIQAAVLAAPGDSLAQAFNITSODDVLFAIFSKQQRK 400  
Qy 347 MKSLDEBALCIFILKQINDRIKEXLSCYRGEGLDIAWKVDDICSSALLTIDNPGC 406  
Db 401 HHPDDSLACAFPIRALNLOIKERLQCYGBGNLWMLGKOVCTKAPVPIIDNPGC 460  
Qy 407 LDMNAPLVSDMVRGIPFTEDRDGMTSVIAYVYKNSIAFVGTSGKLRKIRVDGPRGN 466  
Db 461 LDINQPLGSGTPVGLTYTTSRDRMTSVASYVNGYVVFVGTSGKLRKIRV----- 514  
Qy 467 ALQYE-----TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501  
Db 515 ---YEFRCNAIHLKSKESLLEGSYWMRFNYRQLYFLGEQR 552

RESULT 9  
US-09-904-011-170  
Sequence 170, Application US/09904011  
Publication No. US2003003530A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone

Qy 23 STILTRQAPAPLSOKR-----SFVTRGEPAE- 49  
Db 45 SKLIT--AAPLSMEKQWPMALSVDSVYVLSVWVLAAPAAQMPQFTFHSNRDM 102  
Qy 50 GENHLVDERGTGHLYLGAVNRIRYKLSQDKVLTHTGPDDEDNPKYPPRIYQTCNEPLT 109  
Db 103 TFMHLTVHOGTGAIVYGAIRNRYKLTGNLTIIQVAHKTGPEDNKSRYPLIYQPCSEVLT 162  
Qy 110 TTNVNNKMLIIDYKENVRLIACGSIYOGICCKLRLEDLFLKGPYHKKHEHLSGVNBSGSV 169  
Db 163 LTNVNNKMLIIDYSENRLIACGSIYOGICCKLRLEDLFLIYVSHKHEHLSVNNKTGM 222  
Qy 170 FGVIVSYNLDKLFIAVAVDGKEPEYPTISSRKLTKNSPADGMFAVYHDEFAVSMITK 229  
Db 223 YGVIVRSEGEDEKLFITAVDGKODYPTLSSRKLPRDPSSAMLYELHSDVSSILIKI 282  
Qy 230 PSDFTIIPBDIYVYVGSFGNFFVLTLOPEVNSPPG---STTKBOVYTKVLCKE 286  
Db 283 PSDTALVSHFDIYITGVASGCFVYFLVQPE--TPGVAINSGADLFTTSIVLCKD 340  
Qy 287 DTAFNSYVEVPICERSGVEYRLIQAAVLSKAGAVLGRITGVHPDDLLFTVFSKQQRK 346  
Db 341 DPKFHSYVSLPFGCTFRAGVEYRLIQAAVLAAPGDSLAQAFNITSODDVLFAIFSKQQRK 400  
Qy 347 MKSLDEBALCIFILKQINDRIKEXLSCYRGEGLDIAWKVDDICSSALLTIDNPGC 406  
Db 401 HHPDDSLACAFPIRALNLOIKERLQCYGBGNLWMLGKOVCTKAPVPIIDNPGC 460  
Qy 407 LDMNAPLVSDMVRGIPFTEDRDGMTSVIAYVYKNSIAFVGTSGKLRKIRVDGPRGN 466  
Db 461 LDINQPLGSGTPVGLTYTTSRDRMTSVASYVNGYVVFVGTSGKLRKIRV----- 514  
Qy 467 ALQYE-----TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501  
Db 515 ---YEFRCNAIHLKSKESLLEGSYWMRFNYRQLYFLGEQR 552

Query Match 13.5%; Score 1351.5; DB 10; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3.4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;  
US-09-907-841-170  
ORGANISM: Homo sapiens  
TYPE: PRT  
SEQ ID NO: 170  
LENGTH: 552  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 423

APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,011  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 170  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-011-170

Query Match 13.5%; Score 1351.5; DB 11; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3,4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;  
23 STUTROPAPLSOKR-----SPTFRGEPAR 49  
|||||:|

Db 45 SLLT--AAPLSNEQOPMPRLLENDKRSVLLSVWVLLAPPAKMPQSTFHSNRDM 102  
Qy 50 GFNHLVDERGTGHTYLGAVNRIRYKLSDLKVLVTEHTEGDEDNPKCYPRIVQTCNEPIT 109  
Db 103 TFNHLTVHGTGAVYGAINRIVYKLTGNLTIQVAKTGEEDNKSRYPPLIVQPCSEVLT 162  
Qy 110 TTNVVKMLIDYKERRLLACGSIYOGICRLRLDELFLGSPYKHKHYLSGVNCSGV 169  
Db 163 LTNVVKMLIDYSENRLLACSLYGVCKLRLLDELFLVPSHKHKHYLSGVNKTGM 222  
Qy 170 FGIVASYNLDDKLFATAVDGKPEYFPTISSRKLTQNSADQMPAYVHDFEFAVMKI 229  
Db 223 YGVIVASEGSDGLFGTAVDGKQDYFLLSSRKLPREDSSAMLDYELHSDVFSLLIKI 282  
Qy 230 PSPTFTIIPDPDIYYGSSGNFYFLLOEMNSPPG---STKQVYTSKIVLCKE 286  
Db 283 PSDTLALVSHFDIFYIYGFASGGFYFLVQPE--TPEGVAINSGDLFYTSRIVRLCKD 340  
Qy 287 DTAFSNVEYVEPICSESGVEYRLQAAVYLSKAGAVLGRITGVHPDDLLFTVFSKQGRK 346  
Db 341 DPKFHSVSLPFCCTAGVEYRLQAAVYLSKAGAVLGRITGVHPDDLLFTVFSKQGRK 400  
Qy 347 MKSLDSALCTFLKQINDRIKRLQSCYRGSTLDLAKYKDIKCSALLTIDNPG 406  
Db 401 HHPDDSLACAFPIRAINQIKERLQSCYRGSTLDLAKYKDIKCSALLTIDNPG 460  
Qy 407 LDMNAPLGVSDMVRGIPVTEDEDRMTSVIAYVYKNSIAFYQTSKGLKKTIRVDGPRGN 466  
Db 461 LDINQPLGSGTPVEGLITVTSRDMT SVASIVYNGSVIVFGQTSKGLKKTIRV 514  
Qy 467 ALQYE---TVQVDPGPVLRDMAFSK-DHEQLYMSERQ 501  
Db 515 ---YEFRCNAHILSKESLLEGSYWMRFYRQLYFLGQR 552  
RESULT 10  
US-09-906-742-170  
Sequence 170, Application US/09906742  
Publication No. US20030023054A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Askenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,742  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414









GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,859  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
SEQ ID NO 170  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-859-170

Query Match 13.5%; Score 1351.5; DB 11; Length 552;  
Best Local Similarity 51.6%; Pred. No. 3.4e-114;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;  
23 STLLTQAPAPLSOKOR-----SFTVFRGEPAP- 49  
45 SRLLT--APLSMEQGPMPRALVEDRSVLLSVVLLAPPRAQMPQSTFHSNRM 102  
50 GFMVLVDEKRTGHIYGAVKRIKLSDDLKVLVTHETGDEDNPKYPRIVQTCNEPLT 109  
103 TFMHLTVHQTGVAVYGAIRKVKLTGNLTQVAAHTGPEBDKSRYPVLPVPCSEVL 162  
110 TTNNVNMFLIDYKERNLACGSLYOGICLLRLDELFLKGPBYHKKEHYLSGVNESGV 169  
163 LTNVNMKLLIIDSERNLLACGSLYGVCKLRLDDLFLIVESSHKEHYLSVNTGTM 222  
170 FGIVSYSNLDDYFLATVADGKPEYFPITSSKRLTRNSHADGMFAVFRHDEVAAMIKI 229  
223 YGVIVRSEGRDGLFLGTAVDGKDYFPITSSKRLFRDPSAMLDYELHSDVSSLIKI 282  
230 PSDFTIIPDDIYVYVGFSGNPFYFLTQPEMWSPPG---STKEQVYTSKLVLCKE 286  
283 PSDTLAVSHFPIFYITGPGASGGFYFLTVQPE--TPGVAINAGDLPYTSRLVLCND 340  
287 DTAENSVEVPICGERSGVEYRLLQAAVYSKAGAVIGRTGVHPDDDLFTVFSKQOKR 346  
341 DPKEHSYVSLPFCGTRAGVYRLLQAAVYLAKPDSLAQAFNITSODVFAIYSKQOKY 400  
347 MKSLDESLALCIFILKQNDIKERLOS CVRGEGLDPLAMKVDIPCSSALLTIDNFCG 406  
401 HEPDSDALCAFPRAINLOIKERLOS CVGEGNLEINMLGMDVQCTAPVPIIDNFCG 460  
407 LDNMAPLVGSDMYRGIPVFTEDDRMTSVIAYYKNSLA FVGTKSGKLLKIRVDGGRN 466  
461 LDINQPLGSGTPVEGLFLYTSRDRMTSVASVYVGVTKSGKLLKAVV----- 514  
467 ALQYE-----TVQVVDGCVLRDMAPSK--DHEGLYMSERO 501  
515 ---YFRCSNALHLSKESLIGSVYMKRNYRQULFLGGR 552  
RESULT 15  
US-09-909-204-170  
Sequence 170: Application US/09909204  
Publication No. US20030036061A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: 10466-14  
 / CURRENT APPLICATION NUMBER: US/09/909,204  
 / CURRENT FILING DATE: 2001-07-18  
 / PRIOR APPLICATION NUMBER: PCT/US00/04414  
 / PRIOR FILING DATE: 2000-02-22  
 / PRIOR APPLICATION NUMBER: US 60/143,048  
 / PRIOR FILING DATE: 1999-07-07  
 / PRIOR APPLICATION NUMBER: US 60/145,698  
 / PRIOR FILING DATE: 1999-07-26  
 / PRIOR APPLICATION NUMBER: US 60/146,222  
 / PRIOR FILING DATE: 1999-07-28  
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 / PRIOR APPLICATION NUMBER: PCT/US99/20944  
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 / PRIOR APPLICATION NUMBER: PCT/US99/28313  
 / PRIOR FILING DATE: 1999-11-30  
 / PRIOR APPLICATION NUMBER: PCT/US99/28564  
 / PRIOR FILING DATE: 1999-12-02  
 / PRIOR APPLICATION NUMBER: PCT/US99/28565  
 / PRIOR FILING DATE: 1999-12-02  
 / PRIOR APPLICATION NUMBER: PCT/US99/30095  
 / PRIOR FILING DATE: 1999-12-16  
 / PRIOR APPLICATION NUMBER: PCT/US99/30911  
 / PRIOR FILING DATE: 1999-12-20  
 / PRIOR APPLICATION NUMBER: PCT/US99/30999  
 / PRIOR FILING DATE: 1999-12-20  
 / PRIOR APPLICATION NUMBER: PCT/US00/00219  
 / PRIOR FILING DATE: 2000-01-05  
 / NUMBER OF SEQ ID NOS: 423  
 / SEQ ID NO 170  
 / LENGTH: 552  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / US-09-909-204-170

Query Match 13.5%; Score 1351.5; DB 11; Length 552;  
 Best Local Similarity 51.6%; Pred. No. 3.4e-114;  
 Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

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 DB 45 SRIILT--AAPLSWECQWPWRALEVDRSVLLSVVLLAPPAGMPQFSTFHSNRDW 102  
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 QY 170 FGIYIVSYNDDLLFAITAVDGKPEYFPIISSRKLTKNSEADQMFAIYVPHDEFVASMIXI 229  
 DB 223 YGVIVSEGEDEGLFTGTAVDGKQDYFPIISSRKLPRDESSAMLDYELHSDVFSLSLIXI 282  
 QY 230 PSDFTIIPDFDIYVYVYGFSGNFVFLTLQPEMVSPPG---STREQVYTSKLVRLCKE 286  
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QY 347 MKSLDESALCIFILKQINDRIKERLOSCKYRGEETLDLAWLKVDIPCSSALLTIDNFCG 406  
 DB 401 HHPPDDBALCAFLIRAINLQIKERLOSCKYRGEENLEINWLLGKDVQCTKAPVIDDNFCG 460  
 QY 407 LDMNAPLGVSDMVRGIPVFTEDSDRMTSVIAYYKXHSIAFVGTSGSKLKKIRVDGPRGN 466  
 DB 461 LDINQPLGSGTPEVGLTLYTSRDMTSVASIYVNGISVVFGRKSGKLKRV----- 514  
 QY 467 ALQYE-----TVQVVDGPLYLRDMAFSK--DHEQLYIMSERQ 501  
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 Job time : 53 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 20, 2004, 09:36:12 / Search time 196 Seconds

(without alignments)  
5368.300 Million cell updates/sec

Title: US-09-964-956-13

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Database:

Issued Patents NA.\*  
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5: /cgn2\_6/prodata/2/ina/PTUS.COMB.seg.\*  
6: /cgn2\_6/prodata/2/ina/backfile1.seg.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1359.5	13.6	2477	4	US-09-907-794A-169 Sequence 169, App
2	1359.5	13.6	2477	4	US-09-905-125A-169 Sequence 169, App
3	1359.5	13.6	2477	4	US-09-902-775A-169 Sequence 169, App
4	1349	13.5	4707	3	US-09-181-706-1 Sequence 1, Appl
5	1349	13.5	4707	3	US-09-458-791-1 Sequence 1, Appl
6	1349	13.5	4707	3	US-09-459-066-1 Sequence 1, Appl
7	1349	13.5	4707	4	US-09-459-065-1 Sequence 1, Appl
8	657	6.6	3458	4	US-09-023-655-603 Sequence 603, App
9	629.5	6.3	4626	1	US-08-306-691B-22 Sequence 22, Appl
10	629.5	6.3	4626	5	PCT-US93-06251-27 Sequence 27, Appl
11	323	3.2	2433	4	US-09-300-958A-24 Sequence 24, Appl
12	263	2.6	3524	4	US-09-077-940A-3 Sequence 3, Appl

13	244.5	2.4	3692	4	US-09-077-940A-1 Sequence 1, Appl
14	228.5	2.3	3694	4	US-09-653-274-3 Sequence 3, Appl
15	228	2.3	3261	4	US-09-653-274-5 Sequence 5, Appl
16	227	2.3	2670	1	US-08-121-713D-61 Sequence 61, Appl
17	227	2.3	2670	1	US-08-835-268-61 Sequence 61, Appl
18	227	2.3	2670	2	US-09-060-692-61 Sequence 61, Appl
19	227	2.3	2670	3	US-08-833-391-61 Sequence 61, Appl
20	227	2.3	2670	4	US-09-060-610-61 Sequence 61, Appl
21	227	2.3	2670	5	PCT-US94-10151A-61 Sequence 61, Appl
22	220	2.2	1923	4	US-09-653-274-12 Sequence 12, Appl
23	216.5	2.2	1024	4	US-09-328-475C-37 Sequence 37, Appl
24	207	2.1	2854	1	US-08-121-713D-57 Sequence 57, Appl
25	207	2.1	2854	2	US-08-835-268-57 Sequence 57, Appl
26	207	2.1	2854	3	US-09-060-692-57 Sequence 57, Appl
27	207	2.1	2854	4	US-08-833-391-57 Sequence 57, Appl
28	207	2.1	2854	5	US-09-060-610-57 Sequence 57, Appl
29	207	2.1	2854	5	PCT-US94-10151A-57 Sequence 57, Appl
30	200	2.0	2601	1	US-08-121-713D-53 Sequence 53, Appl
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33	200	2.0	2601	3	US-08-833-391-53 Sequence 53, Appl
34	200	2.0	2601	4	US-09-060-610-53 Sequence 53, Appl
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36	192.5	1.9	3560	1	US-08-121-713D-59 Sequence 59, Appl
37	192.5	1.9	3560	1	US-08-835-268-59 Sequence 59, Appl
38	192.5	1.9	3560	2	US-09-060-692-59 Sequence 59, Appl
39	192.5	1.9	3560	3	US-08-833-391-59 Sequence 59, Appl
40	192.5	1.9	3560	4	US-09-060-610-59 Sequence 59, Appl
41	192.5	1.9	3560	5	PCT-US94-10151A-59 Sequence 59, Appl
42	192	1.9	4157	4	US-08-556-422A-1 Sequence 1, Appl
43	186.5	1.9	2504	1	US-08-121-713D-63 Sequence 63, Appl
44	186.5	1.9	2504	1	US-08-835-268-63 Sequence 63, Appl
45	186.5	1.9	2504	2	US-09-060-692-63 Sequence 63, Appl

#### ALIGNMENTS

RESULT 1  
US-09-907-794A-169 Application US/09907794A  
Sequence 169, Applicant: Genentech, Inc.  
Patent No. 6635468  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flivareff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
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APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,794A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143, 048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145, 698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146, 222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
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PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO: 169  
LENGTH: 2477  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-964-956-169

Alignment Scores:  
Pred. No.: 8.8e-138  
Score: 1359.50  
Percent Similarity: 69.88%  
Best Local Similarity: 53.35%  
Query Match: 13.61%  
Gaps: 7

US-09-964-956-13 (1-1896) x US-09-964-956-169 (1-2477)

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25 LeuLeuThrArgGlnProAlaProLeuSerGlnGlyArgSer-PheValThrPheAr 44  
912 -----GGCCCCCAGAGCGCGCATGCTCTGCTTACACCTTCCA 953  
44 GgLyGluProAlaGlu---GlyPheAsnHisLeuValAlaSpGluArgThrGlyHisI 63  
954 CTTCTAGATCGTGACTGGACCTTCAACACTTGAACCTTCCACAGGAGCGGGGCGGT 1013  
63 eTYrLeuGlyAlaValAsnArgIleTYrIlyLeuSerSerSerLeuValLeuValTh 83  
1014 CTAATGTGGGGCCATCAACCGGCTATPAGCTGACAGGCAACCTGACCATCCAGGAGCC 1073  
83 HisGluThrGlyProAspGluAspAsnProLysCysTYrProProArgIleValGlnTh 103  
1074 TCAATAAGACAGGCGGAGAGAGACACAAGCTCTTACCGGCCCTCATCGAGGCC 1133  
103 rCYsaGluProLeuThr-ThrAsnAsnValAsnLeuMetLeuLeuIleAspTYrIly 123  
1134 CTGAGCGGAAGTCTCACCTCCATCAACAAATGTCAACAAAGTGTCTCATTTGACTACTC 1193

123 sGluAsnArgLeuIleAlaCysGlySerLeuTYrGlnGlyIleCysIlySerLeuArgIle 143  
1194 TGAGAACCGCTGCTGGCTGGAGAGCTTACAGAGGGGTCTGCAAGGCTGCTGCGCT 1253  
143 uGluAspLeuPheLysLeuGlyGluProCysHisLysGlyHisIlyTYrLeuSerGlyVa 163  
1254 GGAATACCTCTTCAATCCCTGGAGGACCATCCACAGAGAGACATACCTGTCAGAGT 1313  
163 lAsnGluSerGlySerValPheGlyValIleValSerTYrSerSerLeuAspLysIle 183  
1314 CAACAGAGCGGACACATGATCGGGGTATGTCCTGAGGGGTGAGATGCGAGACT 1373  
163 uPheIleAlaThrAlaValAspGlyLysProGluTYrPheProThrIleSerSerArgLy 203  
1374 CTTCTATCGCACGCTGTGATGGAGAGACAGATTACTTCCGACCTGTCAGCGCGGA 1433  
203 sLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTYrValPheHisAspGluPheVa 223  
1434 GCTGCCCGAGACCTGATGCTCTACGCCATCTGACATATAGCTACACAGATTCTGT 1493  
223 lAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTY 243  
1494 CTCTCTCTCATCAAGATCCCTTCAAGACCCCTGCGCTGTCTTCCCATTTGACATCTT 1553  
243 rTYrValTYrGlyPheSerSerGlyAsnPheValTYrPheLeuThrLeuGlnProGluMe 263  
1554 CTACATCTACCGCTTGTGATGGGGGCTTGTCTTACTTCTTCACTGTCAGCGCCGAG-- 1611  
263 rValSerProProGly-----SerThrThyIleGlnGlnAlaTYrThrSerLysIle 280  
1612 -----ACCCCTGAGGTGTGGCCATCACTCGCTGGAAGACCTTCTTACCTACGAT 1667  
280 uValArgLeuCysLysGluAspThrAlaPheAsnSerTYrValGluValProIleGlyCY 300  
1668 CGTGGCGCTCTGCAAGATGAGCCCAAGTTCACATACATGTCCTGCTGCTGCTGCTG 1727  
300 sGluArgSerGlyValGlyTYrArgLeuLeuGlnAlaAlaTYrLeuSerLysAlaGlyAl 320  
1728 CACCGCGCGCGGGGAGATATCCGCTCTGAGGCTCTTACCTGCGCAAGCCCTGCGGA 1787  
320 aValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSe 340  
1788 CTCACCTGGCGGAGGCTTCAATATACAGACAGACCATGATCTTGGCATCTTCTC 1847  
340 rLysGlyGlnLysArgLysMetLysSerLeuAspLysSerAlaLeuCYsIlePheIleLe 360  
1848 CAAGGCGGAGAGACATATCACACCCGCGCATACTGCTGCTGCTGCTGCTGCTTAT 1907  
360 uLysGlnIleAspAspArgIleLysGlyArgLeuGlnSerCysTYrArgGlyGluGlyTh 380  
1908 CCGGCGCATCAACTGCAATCAATCAAGAGGCTGAGTCTGTCACAGGGGAGGCA 1967  
380 rLeuAspLeuAlaTrpLeuLysValIleAspIleProCysSerSerAlaLeuLeuThrI 400  
1968 CTTGAGCTCAACTGCTGCTGCTGAGAGAGACCTTCAGAGTGCAGAGAGGCGCTGCCAT 2027  
400 eAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValAspAspMetValAr 420  
2028 GATGATTAATCTTCTGTGAGCTGATCAATCAACAGCCCTGGAGGCTCAACTCAGTGA 2087  
420 GgLyIleProValPheThrGluAspArgArgMetThrSerValIleAlaTYrValTY 440  
2088 GGGCTGACCCCTGTATACACACAGAGGAGCCGATGACTGTGTGCTCTTACGTTTA 2147  
440 rLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysIleArgVa 460  
2148 CAACGGCTACAGGCTGTTTGTGGGACTAAGAGCTGACAGCTGCAAAAAGTAAAGAT 2207  
460 lAspGlyProArgGlyAsnAlaLeuGlnTYrGlu-----ThrValGlnVa 475  
2208 C-----TATGAGTTCAAGATGCTCCATGCCATTCATTCACCT 2240

QY	475	ValAspProdiLyProValIleuArgAspMetalapheserYs---AspHisGluGlnLe	494
	:::	:::	:::
Db	2241	CCTAGCAAAAGACGCCCTCTCTTGGAAGTAGACTATTGTGTGAGATTAACTATAGCAACT	2300
QY	494	uTYrIleMetserGluArgIn 501	
	:::	:::	
Db	2301	TTATTTCCTGGGAAACAAAG 2322	

RESULT 2  
US-09-905-125A-169  
; Sequence 169, Application US/09905125A  
; Patent No. 6664376

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Macher, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,125A  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23069  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20

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: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
:
: SEQ ID NO 169
: LENGTH: 2477
:
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: US-03-905-125A-169

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Alignment Scores:	
Pred. No.:	8, 8e-138
Score:	159, 50
Percent Similarity:	69.88%
Best Local Similarity:	5.33%
Query Match:	12.65%
DB:	4
	7
Length:	2477
Matches:	
Conservative:	271
Mismatches:	84
Indels:	124
Gaps:	31

US-09-964-956-13 (1-1896) X US-09-905-125A-169 (1-2477)

5 ProTTPAsnTrpThrCysLeuSerHisLeuMetValGlyMetGlySerSerThr 24

Db 857 CCCTGGAGGTGGACAGCCGCTCTGTG-GTCCTGCTCTCAGT-GGTCTGGGTGCTGCT--- 91

25 LeuLeuThrArgGlnProAlaProLeuSerGlnIlysgGlnArgSer-PheValIThrPheAr 44

Db 912 -----GGCCCCCAGCAGCCGGCAIGCTCAGTTCAGCACCTTCCA 3'

44 GGLYGLUPTOALAGLU---GLYPHEASHNISLEUVALVALABPGIUTGIMGLYMSL

934 C1C1GAGHAI CG1GAC1GGACCI1VTHCCAC11GGACCG1CACGCCAACCCACCC

[illegible][illegible][illegible]

**0** [0] b B a t e m b e n x x c v y z ] A c c i u c M o t l e u l e u t ] e h s r T v r l y 1 2

1134 CTTCCCTCCTCAACATGTCACAGCTGCATCATGTGACTC 11

133 cG]u]nncnrrat[au]r]ab]aCveg]vSert[euTvrG]ng]vt]eCvsal'ysleuLeuArgIe 14

1194 TGAAGAACCGCTGCTGCTGAGCCTCTACCAAGGGGCTGCAAGCTGCTGCGCT 12

143 uGluAspLeuPheIysLeuGlyGluProTyrHisIysLysGluHisTyrLeuSerGlyVal 16

Db 1254 GGATGACCTCTTCATCCTGGTGGAGCCATCCCAAGAGGACCTACTGTCCAGTGT 13

163 IAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLe 16

Db 1314 CAACAAGCGGCACCATGTACGGGTGATTGTCGCTCTGAGGGTGAGGATGGCAAGCT 13

183 upheilealThrAlaValAspGlyLysProGluTyrPheProThrIleSerSerArgLys 20

Db 1374 CTTCAATCGGACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCCTGTCCAGCCGGA 1'

203 sLeuThrLysAsnSerGluAlaaspGlyMetPheAlaTyrrValPheHisAspGluPheVa 2:

Db 1434 GCTGCCCGAGACCTGAGTCTCAGCCATGCTGCACTATGAGCTACACAGCGATTTCG 1435

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QY      223  lAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleLeu 2
      ... ..

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Db 1494 CTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGTCCTCCACCTTGGACATCTT

Qy 243 rTyVAlTyrgLyphneserSerGlyashpnevAlYrPneLeuInrLeuGInrFICGume 2

[illegible]

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QY 263 tValSerProxiGly-----SerThrThrLySGluGlnValTyrThrSerLeu 280
Db 1612 ----ACCCCTGAGGGTGTGGCCATCACTCCGCTGGAGACCTCTTACCTCAGCAT 1667
QY 280 uValArgLeuGlySGluAspThrAlaPheAsnSerTyrValGluValProIleGly 300
Db 1668 CCGCGCGCTCTGCAAGATGAGCCCAAGTTCACATCAATGCTGCTCCGCGCTTGGGCTG 1727
QY 300 sGluAspSerGlyValGluTyrArgLeuGlnGlnAlaTyrLeuSerValGluVal 320
Db 1728 CACCGCGCGCGGGGTGAATACCGCTCTGAGGCTGCTTACCTGCGCCAGCCCTGGGCA 1787
QY 320 aValLeuGlyArgThrLeuGlyValHisProAspAspAlaLeuPheThrValPhe 340
Db 1788 CTCACCTGGCCAGGCTTCATATATCACCGACGACGATGACTCTTGGCATCTTCTC 1847
QY 340 rLySGlyGlyArgGlyMetLysSerLeuAspGluSerAlaLeuGlyIlePheIle 360
Db 1848 CAAGGGCAGAAAGCATATACACCCGCCAGATGCTGCTGCTGCTGCTTCCCTTCCAT 1907
QY 360 uLySGlnIleAsnAspArgIleLySGluArgLeuGlnSerCysTyrArgGlyGluGly 380
Db 1908 CCGGCGCATCACTTGCAGATCAAGAGGCGCTGCAAGTCTGCTACAGGGCGAGGCGCA 1967
QY 380 rLeuAspLeuAlaTyrPheLeuValIleAspIleProCysSerSerAlaLeuLeuThr 400
Db 1968 CCGGAGGCTCACTGCTGCTGCTGCGGAGGAGCGTCCAGTCAAGAGGCGCTGCTCCAT 2027
QY 400 eAspAspAspPheCysGlyLeuAspMetAsnAlaProLeuGlyValIleSerAspMetVal 420
Db 2028 CCAATGATTACTTGTGGAGCTGACATCAACAGCCCTGGAGGCTCACTCCAGTGA 2087
QY 420 gGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 440
Db 2088 GGGCCCTGACCTGTACACACACACAGCAGGAGCGCATGACTCTGCGCTCTAGCTTGA 2147
QY 440 rLyAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysValArgVa 460
Db 2148 CAACGGCTACAGCGTGTCTTGTGGGACTAGACTGAGCTGCAAAAAGTAAAGCT 2207
QY 460 lAspGlyProArgGlyAsnAlaLeuGlnTyrGlu-----ThrValGlnVa 475
Db 2208 C-----TATGAGTTCAAGATGCTCCAAATGCCATTCACCT 2240
QY 475 lValAspProGlyProValLeuArgAspMetAlaPheSerLys---AspHisGluGlnLe 494
Db 2241 CCTCAGCAAGAGTCCCTCTCTGGAGAGTATGCTATGCTGAGATTAACTATAGCAACT 2300
QY 494 uTyrIleMetSerGluArgGln 501
Db 2301 TTATTTCTTGGGACAAAG 2322

```

RESULT 3  
US-09-902-775A-169  
Sequence 169, Application US/09902775A  
Patent No. 6686451  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.

```

APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCES: 10466-14
CURRENT APPLICATION NUMBER: US/09/902, 775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 169
LENGTH: 2477
TYPE: DNA
ORGANISM: Homo sapiens
US-09-902-775A-169
Alignment Scores:
Pred. No.: 8.8e-138 Length: 2477
Score: 1359.50 Matches: 271
Percent Similarity: 69.88% Conservative: 84
Best Local Similarity: 53.35% Mismatches: 124
Query Match: 13.61% Indels: 31
DB: 4 Gaps: 7
US-09-964-956-13 (1-1896) x US-09-902-775A-169 (1-2477)
QY 5 ProTyrAsnThrPheCysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThr 24
Db 857 CCCTGAGAGTGAAGCGGCTGTGTG-GTCTGCTCTCACT-GATCTGGGTGTCTGCT--- 911
QY 25 LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSer-PheValThrPheArg 44
Db 912 -----GGCCCCCGACGAGCGGCGGATGCCCTGATGTTCAAGCACTTTCCA 953

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QY 44 gglgluProAlaGlu---GlyPheAsnHisLeuValAlaSpGluAlaGThrGlyHisI 63  
Db 954 CTCTAGAGATCGTGTGAGACCTTCAACCACTTGAACCCGACCAAGGAGGGGGCGCT 1013  
QY 63 eTyLeuGlyAlaValAlaAsnArgIleTyLeuSerSerAspLeuValLeuValTh 83  
Db 1014 CTAATGGGGGCGGACCAACCGGGTCTATAGGTGACAGGCAACCTGACATCCAGGTGC 1073  
QY 83 rHisGluThrGlyProAspGluAspAsnProLysCysTyProProAlaGlyIleValGlnTh 103  
Db 1074 TCATAGACAGCGGCGGACAGAGACCAAGCTCTGTTACCGCCCTCATCTGTCAGACC 1133  
QY 103 rCysAsnGluProLeuThrThrThAsnAsnValAsnLeuMetLeuLeuLeuLeuValTy 123  
Db 1134 CTGACAGAGAGTGTCAACCTCAACCAATGTCAACAGGCTGCTCATCTGACTATC 1193  
QY 123 sgluAsnArgLeuIleAlaCysGlySerLeuTyGlnGlyIleCysValLeuLeuArgLe 143  
Db 1194 TGAGAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253  
QY 143 uGluAspLeuPheLeuGlyGluProTyHisLeuGlyHisGlyHisGlyHisGlyHis 163  
Db 1254 GATGACCTCTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313  
QY 163 lAsnGluSerGlySerValPheGlyValIleValSerTySerAsnLeuAspAspValLe 183  
Db 1314 CAACAAGAGCGGACCATCTAGCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373  
QY 183 uPheIleAlaThrAlaValAlaAspGlyLysProGluTyPheProThrIleSerSerArg 203  
Db 1374 CTTCATCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433  
QY 203 sLeuThrLysAsnSerGlyAlaAspGlyMetPheAlaTyValPheHisAspGluPheVa 223  
Db 1434 GCTGCGCGGAGACCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1493  
QY 223 lAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTy 243  
Db 1494 CTCCCTCTCATCAATCACTCTTCAACACCTGCGCTGCTGCTGCTGCTGCTGCT 1553  
QY 243 rTyValAlaTyGlyPheSerSerGlyAsnPheValTyPheLeuThrLeuGlnProGluMe 263  
Db 1554 CTACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1611  
QY 263 rValSerProProGly-----SerThrTyHisGluGlnValTyThrSerLysLe 280  
Db 1612 ---ACCCCTGAGGGGTGTGCGCATCTCCGCTGAGACCTCTTCAACCTCAACGAT 1667  
QY 280 uValArgLeuCysValGluAspPheThrAlaPheAsnSerTyValGluValProIleGlyCy 300  
Db 1668 CGTGCGGCTCTGCAAGATGACCCCAAGTTCATCTCATGCTGCTGCTGCTGCTGCTG 1727  
QY 300 sgluArgSerGlyValGluTyArgLeuGlnAlaAlaTyLeuSerLysAlaGlyAla 320  
Db 1728 CACCGCGGCGGGGTGGAATACCGCTCTGACGCTGCTTCACTGCGCAACCTGCGGA 1787  
QY 320 aValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuPheThrValPheSe 340  
Db 1788 CTCACTGCGCGGCTTCAATATCAACGACCAAGCATGATCTTTGTCATCTTCTC 1847  
QY 340 rLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLe 360  
Db 1848 CAAGGCGGAGAGACAGATCACACCGCGCGGATGACTGCTGCTGCTGCTGCTGCTGCT 1907  
QY 360 uLysGlnIleAsnAspArgIleLysGluTyArgLeuGlnSerCysTyArgGlyGlnGlyTh 380  
Db 1908 CCGGGCGCATCACTTGAATCAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1967  
QY 380 rLeuAspLeuAlaThrLeuLysValIleAspIleProCysSerSerAlaLeuLeuThrI 400  
Db 1968 CTGAGAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2027  
QY 400 eAspAspAsnPheCysGlyLeuAspMetAlaProLeuGlyValSerAspMetValAr 420

Db 2028 CGATGATTACTTCTGTGAGCTGACATCAACGACCCCTGGAGGCTCACTCACTGGA 2087  
QY 420 gglgluProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyValTy 440  
Db 2088 GGCCCTGACCTCTTACACCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2147  
QY 440 rLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysIleArgVa 460  
Db 2148 CAACGCTACAGCGTGTGTTTCTGCGGACTAGACTGCGCACTGAAAAGSTAGAGT 2207  
QY 460 lAspGlyProArgGlyAsnAlaLeuGlnTyGlu-----ThrValGlnVa 475  
Db 2208 C-----TATGAGTTCAGATGCTCCATGCTCAATGCCATTACCT 2240  
QY 475 lValAspProGlyProValLeuArgAspMetAlaPheSerLys---AspHisGluGlnLe 494  
Db 2241 CTGACAGAAAGATCCCTCTTGAAGAGTACTATTGTGTGAGATTAACTATAGGCACT 2300  
QY 494 uTyIleMetSerGlyLysArgGln 501  
Db 2301 TTATTTCTTGGGGAACAAAG 2322

RESULT 4  
US-09-181-706-1  
Sequence 1, Application US/09181706  
Patent No. 6130068  
GENERAL INFORMATION:  
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
APPLICANT: Robert F. Dubose, Richard S. Johnson  
TITLE OF INVENTION: VITRAL ENCODED SEMAPHORIN PROTEIN  
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/181.706  
FILING DATE: October 28, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/958,598 (converted to a  
APPLICATION NUMBER: Provisional, see below)  
FILING DATE: October 26, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: --to be assigned-- (USN 08/958,598  
APPLICATION NUMBER: conversion to Provisional application)  
FILING DATE: October 26, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 470-4189  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

/ HYPOTHETICAL: NO  
 / ANTI-SENSE: NO  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 1..4707  
 / US-09-181-706-1

## Alignment Scores:

Pred. No.:	4,26e-136	Length:	4707
Score:	1349.00	Matches:	480
Percent Similarity:	39.78%	Conservative:	291
Best Local Similarity:	24.77%	Mismatches:	591
Query Match:	13.50%	Indels:	576
DB:	3	Gaps:	74

US-09-964-956-13 (1-1896) x US-09-181-706-1 (1-4707)

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QY 72 TyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrArgIleProAspGluAsp 91
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 TACAGCCTGAGACACAGCCTCTCGCGCTGTACCGGAGCAGCGGCGC----- 235
QY 92 AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 -----AACTGCACAGAGCGGCTCGCTGGCG 282
QY 112 -----AsnAsnValAsnLysMetLeuLeuIleAspTyrLys 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 CCCCCCGGCGGCGCGCGCGCGCGGAGCAGCTTCAGCAAG---CTGCTGCTCCCTTACCGC 339
QY 124 GluAsnArg-----LeuIleAlaCysGlySerLeuTyrGlnGlyIle 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 GAGGGGGCGGCGCGCTCGGGGGGCTGCTCTCACCGGCTGAGACCTTCGACCGGGGGCGCC 399
QY 138 CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGluIleProTyrHisLysLysGlu 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 400 TGGAGGGTGGCGCCCTTGGGCACTG-----AGCCGCAAC 435
QY 158 HisTyrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal 172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 TCCCTGGCGAAGCGGACGAGGTGGTGTGTCGCCACCGCGAGGCTCGACGCGCGCGGTG 495
QY 173 IleValSerTyrSerAsnLeuAspAspLysLeuHelIleAla----- 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 496 GTGTATCCGC---GCCGGCCGGAACAACCGCTGTATCTGGCGGTGGCCGCCACTTACGTG 552
QY 187 -----ThrAla 188
DB 553 CTGCCTGAGCGGAGACGCGGAGCGGTGCAACCCCGCGCATCGACACGACACGAGCGCC 612
QY 189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 613 ATCCGGCTCAAGGACACGAGGCGGCGGAGCTGGCGACGAGCGGTGGGGCGCTCAAG 672
QY 209 GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaSerMetIle 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 673 CTGTCCGAGGCGGCGGAGCGCTGACCTTCGTGAGACGCTTCTCTGGAACGAGAGATC 732
QY 228 LysIleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGly 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 733 TACTTCCCG-----TACTACCCCTACAC 756
QY 248 PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 757 TATACAGCGCGC-----GCTGCCACCGGCTGCGCCACAGCATGGCGCGCATGCG 804
QY 268 GlySerThrThrLysGluGlnValTyrThiSerLysLeuValArgLeuCysLysGluAsp 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 805 CAGAGCACCC-----GAG 816
QY 288 ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu--- 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 817 GTGCTGTTCCAGGC-----CAGGCATCCCTCACTGCGGCGCACGCGCACCCGAGCGC 870
  
```

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QY 307 TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 871 CCGCGCGCTGCTCCTCTCCCGCTGAGGAGCGC----- 906
QY 327 GlyValHisProAspAspLeuPheThrValPheSer-----LysGlyGlnLys 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 907 -----CTGACGCTCGGCGGAGGAGTTCACGCGCGCGCTGAGAGGCG 951
QY 345 ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 952 CAGGAGCGCGCTCCCGCACACAGCGGCGCTGCTCCCTTCAGATATGAGAGATTCAG 1011
QY 365 AspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGlnGlyThrLeuAspLeuAla 384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1012 GCGCGCGCCAGAG-----GTCAGC 1032
QY 385 Trp---LeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAspAsn 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1033 TGGGACTTCAGAGCGCGGAGCCAGCAGCAGCTGCAAGAGCG----- 1071
QY 404 PheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIlePro 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1072 -----GATCAACT-----GAAAGTCCAAACCAATGCCA 1101
QY 424 ValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHis 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1102 TCATCTACTGATGCATTCGACCTGACATCGCTTATGAGACCGGTGATGAAACAG 1161
QY 444 SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysIleArgValAspGlyPro 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1162 ACTGTTTATTTTGGGAGCTGAGAGATGCCATTAAGGTATTTCTT----- 1212
QY 464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal----- 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1213 ---GGTGAATTTGACTTCAATTTGTCAGAGGTTACTGAAATTAAGAAGAGACA 1269
QY 477 -----AspProGlyProValIleLeuArgAspMetAlaPheSerLysAsp 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1270 CCTGTTTTCACAACTCGTTCTGATCTGTG-----AAG 1305
QY 491 HisGluGlnLeuTyrIleLeuSerGluArgGlnLeuThrArgValProValGluSerCys 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1306 AATATCTAATTATTTCTAACAGCTGGGAAGAAGAGAGAAATTCGTGTTCAAACTGC 1365
QY 511 GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTyrCys 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1366 AATTAACATTAATCTGTTCCGAGGTGTTTAAACGACACGACCTTCACCTGCGGTGTC 1425
QY 531 ValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSerGluProArgArg 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1426 CATTGCTCAAAAGTGCTCTTTCAAGAGATTT----- 1461
QY 551 PheAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerVal 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1462 -----GTAATTTCAGAGACTTAANA--- 1482
QY 571 SerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1483 -----ACTGGCTGATATTTCTGCTGGA 1506
QY 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1506 ----- 1506
QY 611 GlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHis 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1507 -----GCAAAAAGTGCCCTTAATTT----- 1527
QY 631 HisValValGlnLeuGlnLeuLysSerLysGluThrArgLysMetThrPheAlaSerThrSer 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1528 -----CAGATATTTGAGAGCAGTAAAGAAAGACTACAGTACTGATGTTGGAGAGC 1578
QY 651 PheValPheTyrAsnCysSerValHisAsnSerCysLeu---SerCysValGluSerPro 669
  
```



Db	1579	TTC-----	-----TCTCCAGACACTCCAAAGTCAGTGCAGATGTGCAGTCTTACG	1626
QY	670	TyrrArgCysHis	TrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer	689
Db	1627	-----	-----AGGAGAGCTCGC-----	1658
QY	690	PheGlnGluGlyArgValIle	ProGluLeuProGluAspCysProGlnLeuArgValAspLys	709
Db	1638	-----	-----	1638
QY	710	IleLeuValProValGluValIle	LeuProIleThrLeuLysAlaLysAsnLeuProGln	729
Db	1639	-----	-----CAGAAATAAAGTCAG-----	1653
QY	730	ProGlnSerGlyGlnArgGlyTyr	GluCysIleLeuAsnIleGlnGlySerGluGlnArg	749
Db	1654	CCCAACCGG-----	-----ACCTGCACCTGTACATC-----	1680
QY	750	ValProAlaLeuArgPheAsnSer	SerSerValGlnCysGlnAsnThrSerTyr	769
Db	1681	-----CCAACCGAGCAACCTTAC	AAAGATGTTTCAGCTTGCAACGATGATCTCTCCTC	1734
QY	770	GluGlyMetGluIleAsnAsnLeu	ProValGluLeuThrValIleThrAsn-----Gly	787
Db	1735	GGTCT-----	-----TGGAAITTTATCAGAC	1755
QY	788	HisPheAsnIleAspAsnProAla	GlnAsnLysValHisLeuTyrLysCysGlyAlaMet	807
Db	1756	AGATTCAACCTTACCAAC-----	-----TGTCTCATCATTA	1785
QY	808	ArgGlnSerCysGlyLeuCysLeu	LysAlaAspProAspPheAlaCysGlyTyrCysGln	827
Db	1786	AAAGAA-----TGCCAGAGCATGGCTA	AAACT-----GGCTGGCGCGGAGTAA	1830
QY	828	GlyProGlyGlnCysThrLeuArg	GlnHisCysProAlaGlnGluSerGlnThrLeuGln	847
Db	1831	AGTGCAAGAAAGGTGT-----	-----	1845
QY	848	LeuSerGlyAlaLysSerLysCys	ThrAsnProArgIleThrGlnIleIleProValThr	867
Db	1846	-----	-----ATCCACCCCTTACA	1860
QY	868	GlyProArgGluGlyGlyThrLys	ValThrIleArgGlyGluAsnLeuGlyLeuGlnIle	887
Db	1861	GCT-----	-----	1863
QY	888	ArgAspIleAlaSerHisValLys	ValAlaGlyValGlnCysSerProLeuValAspGly	907
Db	1864	-----	-----TGGACCCCT-----TCT	1875
QY	908	TyrIleProAlaGluGlnIleVal	CysGluMet-----GlyGluIle	921
Db	1876	GATTATGAGAGAAACCGAAGAC	AGTGTCCAGTGGCTGTCCAGAAAGACATCCAGAGAGAGA	1933
QY	922	LysProSerGlnHisIleAlaGly	PheValGluIleCysValAlaValCysArgProGluPhe	941
Db	1936	AACCCCAAGAGAACAAAGCGG-----	-----AACAGA	1964
QY	942	MetAlaIAspSerSerGlnLeu	TyrTyrPheMetThrLeuThrLeuSerAspLeuPro	961
Db	1963	ACCAACCAAGCTTTAAGGCTCTTAC	-----ATTAAATGTCATTAGACCA	2007
QY	962	SerArgGlyProMetSerGlyGly	ThrGlnValThrIleThrGlyThrAsnLeuAsnAla	981
Db	2008	CAGAAAGTATCGACATTAGGAA	AAAGCAACGTGATGTAACGGGAGCAAACTTTACCGCG	2067
QY	982	GlySerAsnVal-----Val	IleMetPheGlyLysGlnProCys-----	994
Db	2068	GCATCGAACATTCGAAATGATCT	CGAAAGAACAGTAACTGTGATTAAGATGTGATACG	2127
QY	995	LeuPheIleArgArgSerProSer	TyrIleValCysAsnThrThrSerSerAspGluVal	1011

Db 2128 GTTACGCATGTGCTAAATGACACCCACATGAATTCCTCTCCATCAACCGGAAA--- 2188  
 1015 LeuGluMetLeuLys---ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuVal 1033  
 Db 2185 ---GAAATGAAGGATGCTGTGTATCCAGTCTTGATGCTGGAGAACCTGCTTGTGGGATCC 2241  
 1034 PheGlnTyrValGluAspProThrIleValArgIleGlnProGluTyrSerIleValSer 1053  
 Db 2242 TTATCTACATGTTGCTGCCACATGTTGTTCCCTATATTTCTCTACACCATGATAGT 2301  
 1054 GluAsnThrProIleAlaValITPrGlyThrHisIleuAspLeuIleGlnAsnProGlnIle 1073  
 Db 2302 GGTGTCGAAATATATACCATGATGGGAGAAATTTTGTATGTATATGCAAC-----TTA 2355  
 1074 ArgAlaLysHisGlnGlyIleGlnGluIleAsnIleCysGlnValLeuAsnAlaThrGln 1093  
 Db 2356 ATCATTTCCACATGATATTAAGGAAACATATAAGTCTCTAAATATGTGTGGGACTTAC 2415  
 1094 MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGln 1113  
 Db 2416 TCGGGGTTTTTAGCCCCCACTTA----- 2439  
 1114 ArgProGlnGluIupheGlyPheIleLeuAspAsnValGlnSerLeuIleLeuAsnLys 1133  
 Db 2440 -----AAGAGTTCAAAAGATGCGCACAAATGTCCTGTGAGCTGAGAGAGACAAAGAC 2490  
 1134 Thr-----AsnPheThrTyrProAsnProValPheGluAlaPheGly 1148  
 Db 2491 ACCTACTTGATTTGTGGAACCTTCGACATATTCGGAGAGACCCCAAGATTCAGGGGTATCGG 2550  
 1149 ProSerGlyIleuGlnLeuLysProGlyThrProIleIleuLysGlyLysAsnLeu 1168  
 Db 2551 -----GTGGATCCGAGGTGAGACACAAATGTGAAGTGAAGAAATTCAA----- 2592  
 1169 IleProValAlaGlyGlyAsnValIleLeuAsnTyrThrValLeuValGlyGlnLys 1188  
 Db 2593 -----AAGAAATGACAACTTCATATTTCCAAAAA 2625  
 1189 ProCysThrValThrVal-----SerAspValGlnLeuLysCysGlnSerProAsn 1205  
 Db 2626 GACATTGAATTAATTAATCTCTTCATCGAGGAAAAATGGCAATTAAATTCAGTTTGAAAT 2685  
 1206 LeuIle----- 1207  
 2686 ATTACTGAATCAAGATCTTACACCATCTTTGCAAAATTAAAGCATCAAGACTGCA 2745  
 1208 -----GlyArgHisIleValMetAlaArgValGlyGlyMetGlyTyrSer 1222  
 Db 2746 AGCACCATTCGCCAATCTTCTTAAGAAAGTTGGGTCAAGCTGGGAAAACTGGAG----- 2799  
 1223 ProGlnMetValTyrIleAlaProAspSer---ProLeuSerIeuProAlaIleValSer 1241  
 Db 2800 -----CTCTAGCTGAGACAGAGACATCTTCCATCATAGTATTTTCTGATTGTG 2850  
 1242 IleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLys 1261  
 Db 2851 CTCCTGTGC-----TTGCTAGTGTGATTTCTCAATTTTGGCGCGGTGGGGGTGACACAG 2901  
 1262 ArgLysSerArgGlnSerAspLeuThrLeuLysArgLeuGlnMetGlnMetCaspAsnLeu 1281  
 Db 2902 CACAAATCGAAGAG-----CTGAGTGGCAAAACAGAGTCAA---CAACTGAATTTGCTG 2952  
 1282 GluSerArgValAlaLeuGlnCysLysGlnAlaPheAlaGluLeuGlnThrAspIleHis 1301  
 Db 2953 GAAACCGAGCTCCGGAAGAGATACGTACCGCTTTGCTGAGCTGCAGATGGAATGAATG 3012  
 1302 GluLeuThrSerAspLeuAspGlyAlaGly---IleProPheLeuAspTyrArgThrTyr 1320  
 Db 3013 GATGTG-----GTTGATAGTTTGGAACTGTTCCCTTCCTTGATCAAAACATTTT 3063  
 1321 ThrMetArgValLeuPhePro-----GlyIleGluAspHisProValIleArgAspLeu 1338  
 Db 3064 GCTCTGAGAACTTTTCTCCCTGAGTCAGGTGGCTTACCCACCATTTTCACTGAAGAATATG 3122



TELEPHONE: (206) 470-4189  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4707 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..4707  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-458-791-1

Alignment Scores:  
 Pred. No.: 4,26e-136 Length: 4707  
 Score: 1349.00 Matches: 480  
 Percent Similarity: 39.78% Conservative: 291  
 Best Local Similarity: 24.77% Mismatches: 591  
 Query Match: 13.50% Indels: 576  
 Gaps: 74

US-09-964-956-13 (1-1896) x US-09-458-791-1 (1-4707)

QY 72 TyrLysLeuSerSerAspLeuLysValLeuValThiHsGluThrGlyProAspGluAsp 91  
 DB 208 TACAGCTTGAGAGACAGAGCTCTGCGCTGTACCGGAGACCAACCGGCGC----- 255  
 QY 92 AspProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThrThr 111  
 DB 256 -----AACTGCACAGAGCGGCTCTCGCGGCG 282  
 QY 112 -----AsnAsnValAsnLysMetLeuLeuIleAspTyrLys 123  
 DB 283 CCCCCCGCGGCGCGCGCGCGCGGAGAGAGCTTCAGCAAG--CTGCTGTGCTGCCCTACCGC 339  
 QY 124 GluAsnArg-----LeuIleAlaCysGlySerLeuTyrGlnGlyIle 137  
 DB 340 GAGGGGGCGCGCGCGCTCGGGGGGCTGCTCTCAGCGCGCTTCAGCACTTCACCGGCGCGCG 399  
 QY 138 CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyLubProTyrHisLysLysGlu 157  
 DB 400 TGGAGAGTGGCGCGCGCTGGGCAACCTG-----AGCCGCAAC 435  
 QY 158 HisTyrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal 172  
 DB 436 TCCCTGGCAACCGGACCGAGGTGTGTCTGTCACCGGAGGCTGACGCGCGCGGTG 495  
 QY 173 IleValSerTyrSerAsnLeuAspAspLysLeuPheIleAla----- 186  
 DB 496 GTGACCGG---GGGGCGCGGAAACACACGCTGTGACTGCGGTGGCGCGGCACTACGTG 552  
 QY 187 -----ThrAla 188  
 DB 553 CTGCCTGAGCGGAGAGCGGAGCGGAGCGGCTGCAACCGCGGCACTTCAGCAACGAGCGGC 612  
 QY 189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208  
 DB 613 ATCCCGCTCAAGAGACAGGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 672  
 QY 209 GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal--AlaSerMetIle 227  
 DB 673 CTGTGCAAGGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 732  
 QY 228 LysIleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGly 247  
 DB 733 TACTTCCC-----TACTACCCCTTACAC 756  
 QY 248 PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro 267

DB 757 TATACAGCGCGC-----GCTGCACCGCGCTGGCCGAGCATGGCGCATCGCG 804  
 QY 268 GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp 287  
 DB 805 CAGAGCACAC-----GAG 816  
 QY 288 ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu--- 306  
 DB 817 GTGCTGTTCAGGCG-----CAGGACATCCCTGACTGCGGCGGAGCGGAGCGGAGCGG 870  
 QY 307 TyrArgLeuLeuGlnAlaAlaTyrLysSerLysAlaGlyValValLeuGlyArgThrLeu 326  
 DB 871 CGCGCGCTGCTCTCTCTCCAGCTGAGTGAAGCC----- 906  
 QY 327 GlyValHisProAspAspLeuPheThrValPheSer-----LysGlyGlnLys 344  
 DB 907 -----CTGACGCTTGGCGGAGGAGTTCAGCGCGCGCGCGCGCGCGCGCGCG 951  
 QY 345 ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 364  
 DB 952 CAGAGAGCGGCGCTCCCGCACACACGCGGCTCTGCTCTTCAAGATGAGTGAATCAG 1011  
 QY 365 AspArgIleLysGluArgLeuGlnSerCysTyrArgIleGluGlyThrLeuAspLeuAla 384  
 DB 1012 GCGCGCGCCAGAGG-----GTCAGC 1032  
 QY 385 Tyr-----LeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAsn 403  
 DB 1033 TGGAGCTTCAAGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1071  
 QY 404 PheCysGlyLeuAspMetAlaProLeuGlyValSerAspMetValArgGlyIlePro 423  
 DB 1072 -----GATCAACCT-----GAAAGAGTCAACCAATTCGA 1101  
 QY 424 ValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHis 443  
 DB 1102 TCATCTACTTCATTCATTCGAGCTGACCTGACATTCCTTTATGACACCGTGTATGATACAGG 1161  
 QY 444 SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleAlaGlyValAspGlyPro 463  
 DB 1162 ACTGTTTATTCCTGGGAGCTGAGATGGCCAGTACTTCAAGTATTCCTT----- 1212  
 QY 464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal----- 476  
 DB 1213 ---GCTGGAATTGACTTCAATTCGACAGAGTTTCTATGAAATTAAGAAGAGCA 1269  
 QY 477 -----AspProGlyProValLeuArgAspMetAlaPheSerLysAsp 490  
 DB 1270 CCGTTTCTCAAACTGCTCTGATCCTGTG-----AAG 1305  
 QY 491 HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCys 510  
 DB 1306 AATATCTCAATTCATCAACGCTGGGAAAGAGTGAAGAAATTCGTTTCAAACTGC 1365  
 QY 511 GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTyrCys 530  
 DB 1366 AATAAACAATAATCTGTCGAGAGTGTAAACAGCACAGCCCTGCGGTGTGTGC 1425  
 QY 531 ValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSerLysGluProArgArg 550  
 DB 1426 CATTCGCTCAAAAGGTGACTTTCAGAGATGT----- 1461  
 QY 551 PheAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerVal 570  
 DB 1462 -----GTAACATTCAGAGAACTTGAA--- 1482  
 QY 571 SerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 590  
 DB 1483 -----ACTGAGCTGATATTCGCTGCA 1506  
 QY 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610  
 DB 1506 ----- 1506

QY 611 GlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGlnAsnGlyAspHis 630  
 DB 1507 -----GCAAAAAGTGGCCCTAAATTT----- 1527  
 QY 631 HisValValGlnLeuGlnLeuLysSerIleGluThrGlyMetThrPheAlaSerThrSer 650  
 DB 1528 -----CAGATTAATTGCAAGCATTAAGAAAAGACTACAGTACTACTGTGGGAGAGC 1578  
 QY 651 PheValPheTyrAsnCysSerValHisAsnSerCysLeu--SerCysValGlnSerPro 669  
 DB 1579 TTC-----TTCCTCAAGACACTCAAAAGTCATGGTGAAGAAATGTGCACTTACG 1626  
 QY 670 TyrArgCysHisTyrCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 689  
 DB 1627 -----AGGAGAGCTCTGC----- 1638  
 QY 690 PheGlnGluGlyArgValLysLeuProGlnAspCysProGlnLeuLeuArgValAspLys 709  
 DB 1638 ----- 1638  
 QY 710 IleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeuProGln 729  
 DB 1639 -----CAGATTAATAAGTCAG 1653  
 QY 730 ProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArg 749  
 DB 1654 CCAACACCG-----ACCTGCACCTGTACATC----- 1660  
 QY 750 ValProAlaLeuArgPheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyr 769  
 DB 1661 -----CCACCAAGACCACTACAAAGATGTTTCAGTTCGACAGTGTCTCTCTC 1734  
 QY 770 GluGlyMetGlnIleAsnAsnLeuProValGluLeuThrValValTyrAsn-----Gly 787  
 DB 1735 GGTTC-----TGAATTTATCAGAC 1755  
 QY 788 HisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMet 807  
 DB 1756 AGATTCAACTTACCAAC-----TGCTCATCTATTA 1785  
 QY 808 ArgGlnSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTyrCysGln 827  
 DB 1786 AAAGAA-----TGCCCAAGCATGCGTAGAACT-----GGCTGGCGCTGGGTGAAA 1830  
 QY 828 GlyProGlnGlnCysThrLeuArgGlnHisCysProAlaGlnGlnSerGlnTyrLeuGln 847  
 DB 1831 AGTGCAGAAAGCTG----- 1845  
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 DB 1864 -----TGGGACCC-----TCT 1875  
 QY 908 TyrIleProAlaGlnIleValCysGluMet-----GlyGluAla 921  
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Qy      1357 GlnLeuIleAsnAsnValPheLeuLeuSerPheIleArgThrLeuGlnSerGlnArg 1376
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Qy      1631 ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGlnSerGlyValLys 1650

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Qy      1709 LeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGlnGlnAlaAspLysHisGly 1728
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RESULT 6
US-09-459-066-1
Sequence 1, Application US/09459066
Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: Spitzers, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066

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FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/958,598  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Henry, Janis C.  
 REGISTRATION NUMBER: 34,347  
 REFERENCE/DOCKET NUMBER: 2631  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 470-4189  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4707 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..4707  
 US-09-459-066-1  
 Alignment Scores:  
 Pred. No.: 4.26e-136 Length: 4707  
 Score: 1349.00 Matches: 480  
 Percent Similarity: 39.78% Conservative: 291  
 Best Local Similarity: 24.77% Mismatches: 591  
 Query Match: 13.50% Indels: 576  
 DB: 3 Gaps: 74  
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 DB 256 -----AACTGCACAGAGCGCGGTCTGCTGCGC 282  
 QY 112 -----AsnAsnValAsnIysMetLeuLeuLeuAspTyrTys 123  
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 QY 124 GluAsnArg-----LeuIleAlaCysGlySerLeuTyrGlnGlyIle 137  
 DB 340 GAGGGGGCGCGCGCGCTGCGGGGGCTGCTGCTACCGGCTGACCTTCGACCGGGGGCGC 399  
 QY 138 CysIysLeuLeuArgLeuGluAspLeuPheIysLeuGlyGluProTyrHisIysIysGlu 157  
 DB 400 TCGAGGAGCGCGCGCGCTGGGCAACTG-----AGCGCGAAC 435  
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 Db 1507 -----GCAAAAGAGCCCTTAAT 1527  
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 Db 2626 GACATTTGAATTAATCTCTTCATCGGGAATAATGGCAATTAATTCAGTTTGAATAAT 2685  
 QY 1206 LeuIle----- 1207  
 Db 2686 ATTACTGAATCAAGATCTTACCACTCTTGCATAAATTAAGGCATCAAGACTGCA 2745  
 QY 1208 -----GlyArgHisLysValMetAlaArgValGlyGlyMetGlyTyrSer 1222  
 Db 2746 AGCACCATTTGCCAATCTTTAGAAAGTTGGGTCAAGCTGGAAACCTGGAG----- 2799  
 QY 1223 ProGlyMetValTyrIleAlaProAspSer---ProLeuSerLeuProAlaIleValSer 1241  
 Db 2800 -----CTTACGTGACAGAGAGTCAAGTCTTCCACATGATTTTTCATTTGTG 2850





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COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,065
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4707
US-09-459-065-1

Alignment Scores:
Pred. No.: 4,266-136 Length: 4707
Score: 1349.00 Matches: 480
Percent Similarity: 39.78% Conservative: 291
Best Local Similarity: 24.77% Mismatches: 591
Query Match: 13,504 Indels: 576
DB: Gaps: 74

US-09-964-956-13 (1-1896) x US-09-459-065-1 (1-4707)
QY 72 TyTLeuSeSerSeSerLeuValLeuValThriGluThriGlyProAspGluAsp 91
DB 208 TACAGCTGAGACAGACGCTCTGCGCGGTACCGGACCAAGCGGC----- 255
QY 92 AsnProLyCySerProProArgIleValGlnThiCyAsnGluProLeuThiThr 111
DB 256 -----AACTGCACAGAGCGGCTCTGCGGCG 282
QY 112 -----AAsnValAsnLysMetLeuIleAspTyrLys 123
DB 283 CCCCCCGCGCGCGCGCGCGCGAGACGCTTACGACAG-----CTGCTGCGCCCTAACCGC 339
QY 124 GluAsnArg-----LeuIleAlaCySerLysSerLeuTyrGlnGlyIle 137
DB 340 GAGGAGGCGCGCGCGCTCGGCGGCTGCTGCACCGCGCTTCGACCGGCGCGCC 399
QY 138 CyLysLeuLeuLysArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGlu 157
DB 400 TGGAGAGTGGCGCGCGCTGGGCAACCTG-----AGCCCAAC 435
QY 158 HisTyrLeuSerGlyVal-----AsnGlnSerGlySerValPheGlyVal 172
DB 436 TCCCTGGCAACGCGACCGAGTGTGTCTGTCACCGCGAGCGGTGACGCGCGCGTGT 495
QY 173 IleValSerTyrSerAsnLeuAspLeuLysLeuPheIleAla----- 186
DB 496 GTGTACCGC---GCGGCGCGGACACCGCTGGTGGTGGCGGCGCGCGCACTTACGTG 552

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QY 187 -----ThrAla 188
DB 553 CTGCTGAGCGGAGACGGGAGCCCTGCGACCCCGGACATCCAGCACGACGCGCC 612
QY 189 ValAspGlyLysProGluTyrPheProThiLysSerAspGlyLeuThiLysAsnSer 208
DB 613 ATCGCGGTCAAGACACGAGCGGCGCGCGAGCTGCGACAGAGAGCTGGGCGCGCTCAAG 672
QY 209 GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaSerMetIle 227
DB 673 CTGTCGAGGCGCGCGCGCGCTGCACTTCGTGGAGCGCTTCTCGAAGCGGACATC 732
QY 228 LysIleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGly 247
DB 733 TACTTCCC-----TACTACCCCTCAAC 756
QY 248 PheSerSerGlyAsnPheValTyrPheLeuThiLeuGlnProGluMetValSerProPro 267
DB 757 TATACGAGCGGC-----GCTGCCACCGGCTGGCCCGACATGGCGCGCATCGC 804
QY 268 GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCyLysGluAsp 287
DB 805 CAGAGCAC-----GAG 816
QY 288 ThrAlaPheAsnSerTyrValGluValProIleGlyCySerGluArgSerGlyValGlu--- 306
DB 817 GTGCTGTCCAGGCG-----CAGGCATCCCTGCACTGCGCGCACCGCGCCAGCGCGC 870
QY 307 TyrArgLeuLeuGlnAlaIleTyrLeuSerTyrAlaGlyValValLeuGlyArgThrLeu 326
DB 871 CGCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 327 GlyValHisProAspAspAspLeuLeuPheThrValPheSer-----LysGlyGlnLys 344
DB 907 -----CTGACGCTGCGCGGAGTGTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 951
QY 345 ArgLysMetLysSerLeuAspGluSerAlaLeuCySerIlePheIleLeuLysGlnIleAsn 364
DB 952 CAGGAGCGGCGCTCCCGCACCGACCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1011
QY 365 AspArgIleLysGluArgLeuGlnSerCySerTyrArgGlyGluGlnThiLeuAspLeuAla 384
DB 1012 GCGCGCGCGCAAGCG-----GTCAGC 1032
QY 385 Trp---LeuLysValLysAspIleProCySerSerAlaLeuLeuThiLysAspAsn 403
DB 1033 TGGACCTTCAAGACGCGCGAGCGCACTGCAGAGAGG----- 1071
QY 404 PheCySerGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIlePro 423
DB 1072 -----GATCAACCT-----GAAAGAGTCCAAACCAATCGCA 1101
QY 424 ValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHis 443
DB 1102 TCATCTACCTTGAATCCATTCGATCGATCAATCCGTTTATGCGACCGGTGTAATGAGACG 1161
QY 444 SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyPro 463
DB 1162 ACTGTTTATCTTGGGAGCTGAGAGTCCAGTACTTAAAGTATTCTT----- 1212
QY 464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnValAl----- 476
DB 1213 ---GATGAGATTGACTTCAATTCGACAGAGCTTATCATGAAATTAAAGAGAGACA 1269
QY 477 -----AspProGlyProValLeuArgAspMetAlaPheSerLysAsp 490
DB 1270 CCTGTTTCTCAACACTGCTCTGATCTGTG-----AAG 1305
QY 491 HisGlnGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGlnSerCyS 510
DB 1306 AATATCTACATTATCTTAACAGCTGTGGAGAGAGGTGAGAGAAATTGCTGTGCAACATGCG 1365
QY 511 GlyGlnTyrGlnSerCyGlyGluCyLeuGlySerGlyAspProHisCyGlyTyrProCyS 530

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Db      1366 AATAAACAATAATCTGTTCCGAGGCTTTACAGACAGACCCCTGCTGCGTTGGTGC 1425
      531 ValLeuH:saenTh:cyethrArglysluArgCysGlyuArgSerLySgluProArgArg 550
Db      1426 CATTGCTACAAAGGTGACCTTTTCAGAGAGATTGT----- 1461
      551 PheAlaSerGluMetLySgluCysValArgLeuThrValHisProAsnAsnIleSerVal 570
Db      1462 -----GTCATTCAGAGAACTTGAA--- 1482
      571 SerGlnTyraSnaValLeuValLeuGluThrTyraSnaValProGluLeuSerAlaGly 590
Db      1483 -----AACTGCTGAGATATTCGCTGCA 1506
      591 ValAenCyThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610
Db      1506 ----- 1506
      611 GlnCyTySerProAlaAlaLySgluValProArgIleIleThrGluAsnGlyAspHis 630
Db      1507 -----GCAAAAAAGTCCCTAAATT----- 1527
      631 HisValValGlnLeuGlnLeuLySerLySgluThrArgLyMetThrPheAlaSerThrSer 650
Db      1528 -----CAGATATATTCGAGCAGTAAAGAAAGAACTACAGTACTATGCTGGAGAGC 1578
      651 PheValPheTyraSnaCysSerValHisAsnSerCysLeu---SerCysValGluSerPro 669
      1579 TTC-----TCTCCAGACACCTCAAGCTCATGTGAGAGAAATGCGACTCTAGC 1626
      670 TyraGCSnH:trpCysLeuTyraGhiSvalCysThrHisAspProLySgluThrCysSer 689
Db      1627 -----AGGAGCTCTGC----- 1638
      690 PheGlnGluGlyArgValLyLeuProGluAspCysProGlnLeuValArgValAspLys 709
Db      1638 ----- 1638
      710 IleLeuValProValGluValIleLySProIleThrLeuLysAlaLyAsnLeuProGln 729
Db      1639 -----CAGAAATMAAGTCAAG 1653
      730 ProGlnSerGlyGlnArgGlyTyrcylCysIleLeuAsnIleGlnLySerGluGlnArg 749
Db      1654 CCCAACCGG-----ACCTGCACCTGACATC----- 1680
      750 ValProAlaLeuArgPheAsnSerSerValGlnCysGlnAsnThrSerTySerTy 769
      1681 -----CCAAACGAGCAACTACAAAGATGTTTCAGTGTGCACAGTATGTTCCCTTC 1734
      770 GluGlyMetGlnIleAsnAsnLeuProValGluLeuThrValValTyrAsn-----Gly 787
Db      1735 GGTTCT-----TGAATTATTCAGAC 1755
      788 HisPheAsnIleAspAsnProAlaGlnAsnLySValHisLeuTyLyCysGlyAlaMet 807
Db      1756 AGATTCACTTACCAAC-----TGCTCATCATTA 1785
      808 ArgGluSerCysGlyLyLeuCySleuLySAlaAspProAspPheAlaCysGlyTyrProGln 827
Db      1786 AAAGAA---TGCCACGACATGCGTAGAAACT-----GGCTGCGCGTGGGTAA 1830
      828 GlyProGlyGlnCyethrLeuArgGlnHisCysProAlaGlnGluSerGlnTyrLeuGlu 847
Db      1831 AGTGCAAGAAGGT----- 1845
      848 LeuSerGlyAlaLySerLySctThrAsnProAlaGlieThrGluIleIleProValThr 867
Db      1846 -----ATCCACCCCTTACA 1860
      868 GlyProArgGluGlyGlyThrLySValThrIleArgGlyGluAsnLeuGlyLeuGluPhe 887

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Db      1861 GCT----- 1863
      888 ArgAspIleAlaSerHisValLySValAlaGlyValGluCysSerProLeuValAspGly 907
Db      1864 -----TGGACCT-----TCT 1875
      908 TyrIleProAlaGluGlnIleValCysGluMet-----GlyGluAla 921
      1876 GATTATGAGAGAAACCAAGACAGTGTCCAGTGGCTGTGAGAGACATCAGAGAGAGA 1935
      922 LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe 941
Db      1936 AGACCCAGAGAGACAGGG-----AAAGCA 1962
      942 MetAlaArgSerSerGlnLeuTyTyrcylPheMetThrLeuThrLeuSerAspLeuLysPro 961
      1963 ACCAACGAGCTTACAGGCTTCTAC-----ATTAAGTCATGAGCCA 2007
      962 SerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuSnaIle 981
      2008 CAGAAAGTATGCACATTAGGAGAAAGCAACGTGATGTAACGGAGCAAACTTTACCCGG 2067
      982 GlySerAsnVal---ValValMetPheGlyLySgluProCys----- 994
      2068 GCATGACATCATCATATGATCCGAAAGAACACAGTACTGTGATAGAGATGTGATACAG 2127
      995 LeuPheHisArgArgSerProSerTyrrIleValCysAsnThrThrSerSerAspGluVal 1014
      2128 GTTACGCAATGTGTAAATATACACCCACATGAATTTCTCTTCATCAAGCCGGAAA--- 2184
      1015 LeuGluMetLys---ValSerValGlnValAspArgAlaLySleHisGlnAspLeuVal 1033
      2185 ---GAATGAAGATGTGTATCCAGCTTGATGGTGGGAAGTGCCTTCTGGGATCC 2241
      1034 PheGlnTyraValGluAspProThrIleValArgIleGluProGluTyrSerIleValSer 1053
      2242 TTATCCTAATTCCTGTCGACATGTTGCTCCATTATTTCCGTAACCCGATGACAT 2301
      1054 GlyAsnThrProIleAlaValArgLyThrHisSleuAspLeuIleGluAsnProGlnIle 1073
      2302 GGTGTCMAAATTAACATGATGGCAGAAATTTGATGTAATTGACAAAC-----TTA 2355
      1074 ArgAlaLyHisGlyLySgluHisIleAsnIleCysGluValLeuSnaIleThrGlu 1093
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      1094 MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu 1113
      2416 TCGGGGTTTAAACCCCAAGTTA----- 2439
      1114 ArgProGluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLys 1133
      2440 -----AAGAGTTCAAAAGTGCACCAATGTCACTGTGAAGCTGAGAGTCAAGAC 2490
      1134 Thr-----AsnPheThrTyTyrcylProAspProValPheGluAlaPheGly 1148
      2491 ACCTACTTGATGTGGAACCTGCAGTATCGGAGAGACCCAGATTCACGGGATTCGG 2550
      1149 ProSerGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLySgluTyraSnaLeu 1168
      2551 -----GTGAAATCCGAGTGCAGACAGAACTGAGTGAATAATTCA----- 2592
      1169 IleProProValAlaGlyLeuSnaValLySleuAsnTyThrValLeuValGlyGluLys 1188
      2593 -----AAAGAAATGACACTTCAATATTTCCAAADA 2625
      1189 ProCysThrValThrVal-----SerAspValGlnLeuLysCysGluSerProAsn 1205
      2626 GACATTTGAATATTCCTCTTCCATGGGGAATGCGCAATTAATTCAGATTGTAATAT 2685
      1206 LeuIle----- 1207
      2686 ATTACTAGAAATCAAGATCTTACCAACCATCTTTCGAAAATTAAGGCATCAAGACTGCA 2745

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QY 1208 -----GlyArgHisValMetAlaArgValGlyMetGluTyrSer 1222  
 Db 2746 AGCAGCATGCCAAGCTCTTAAGAAAGTTCGGGTCAAGCTGGAAAGCTGAG----- 2799  
 QY 1223 ProGlyMetValTyrTleAlaProAspSer---ProLeuSerLeuProAlaIleValSer 1241  
 Db 2800 -----CTCTACGTCGAGCAGAGTCAAGTCTTCCTCCACATGGATTTCTGATTGTG 2850  
 QY 1242 IleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLys 1261  
 Db 2851 CTCCTGTC-----TTGCTAGGATGTTGATTTTGGCGCGGTGGGTGACCAAG 2901  
 QY 1262 ArgLysSerArgGlySerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281  
 Db 2902 CACAAATCGAAGAG-----CTGAGTCCGCAAAACAGAGTCAA---CAACTGAATTTGCTG 2952  
 QY 1282 GluSerArgValAlaLeuGlnCysLysGlyAlaPheAlaGluLeuGlnThrAspIleHis 1301  
 Db 2953 GAAAGGAGCTCCGAAAGAGATACGTACGGCTTTGAGCTGCAGTGAATTAATTG 3012  
 QY 1302 GluLeuThrSerAspLeuAspGlyAlaGly---IleProPheLeuAspTyrArgThrTyr 1320  
 Db 3013 GAGGTG-----GTTGATGATTGGAACGTGCTCCCTTCCTGACTACAAACATTTT 3063  
 QY 1321 ThrMetArgValLeuPhePro-----GlyTleGluAspHisProValLeuArgAspLeu 1338  
 Db 3064 GCTCTAGAACCTTCTTCCCTGAGTGGCTTCAACCAATCTTCACTGAAGATATG 3123  
 QY 1339 GluValProGlyTyrArgGlnGluArgValGlyLysGlyLeuLysLeuPheAla----- 1356  
 Db 3124 -----CATAAACAGAGAGCGCAACAGCAAGAAATGAAGTCAACACTTTGGAT 3171  
 QY 1357 GluLeuIleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGlnSerGlnArg 1376  
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 QY 1417 LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys 1436  
 Db 3352 -----AGTAACTGACCGCGAAGACTGATGCTGAGCGACGAGTCCGTCCAAATA 3405  
 QY 1437 MetLeuThrAsnTyrPheThrPheLeuLeuTyrLysPheLeuLysGlnCysAlaGlyGln 1456  
 Db 3406 CTCCTCAAAACTGGATGTCGTCGCTTCTGATTTCTCCGGAGACTGCGGAGAG 3465  
 QY 1457 ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGlnLysGlyProIleAspAla 1476  
 Db 3466 CCTTCTATTGTGTGAGCAGCTGGAACCAAGAAATTAACAGGGTCCCGGAGTGA 3525  
 QY 1477 IleThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAsp 1496  
 Db 3526 ATCACTTGCAAAAGCCCTGTACACACTTAATGAAGATGAGTGTGTGGAGGTTCGGAA 3585  
 QY 1497 TyrLysThrLeuValLeuSerCysVal-----SerProAspAsnAlaAsnSerPro 1513  
 Db 3586 TTCAGTACTGTGCATTAACGTCGCTTTGAAAAAATCCCGGAAAAACAGAGGTGAGAT 3645  
 QY 1514 -----GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGln 1530  
 Db 3646 GTCTGTGGAATATTTCAATGATGTTCTGACTGTGAGACCACTTGCCCAAGCAAGAA 3705  
 QY 1531 LysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaIleAsp 1550  
 Db 3706 AAGATTTTCCAGCATTTTAAACAAAAATGAGCTCTCTTATGAGACTTGAAGTTATGA 3765

QY 1551 MetAspLeuGlnTyrPargGlnLysSerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570  
 Db 3766 ATGGCTCTTGAAGCTTCAATGGGACACAGCAAGAAAGAACTTCTGACATCGCAAGATTC 3825  
 QY 1571 ThrThrLysIleGlnAsnAspTyrPylsArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590  
 Db 3826 TCGGTGATTTGTGAAGTGAATGCAACCACTTAACCAACATTTGGCCACTGTGAGATATCA 3885  
 QY 1591 AspGlySerValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn 1610  
 Db 3886 AATGATTCACATTAATAAGTC----- 3906  
 QY 1611 SerThrValSerArgThrSerAlaSerLysTyrGlnLysMetIleArgTyrThrLysSer 1630  
 Db 3907 -----TTTAAGAGATGACCAAAATTTACTTCAAT 3936  
 QY 1631 ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGlnSerGlyValLys 1650  
 Db 3937 GTGAGATGACTGGATGACCACTGCATTTGATTTTACAGATTCGAGCA----- 3987  
 QY 1651 MetTyrHisLeuValLysAsnHisGluHisGlyAspGlnLysGluLysAspArgLysSer 1670  
 Db 3988 ---TTCAGATGTGCAGAGAAAGAGACAT-----CGAGGAG 4023  
 QY 1671 Lys-----MetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeu 1688  
 Db 4024 CACAGTTCAAAGTAAAGAAATGATNCTGACAAAGCTGCTGTCGACCAAGTGGCAATT 4083  
 QY 1689 GlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisAlaGlySerAla 1708  
 Db 4084 CATCTGTGCTGTAATAAATTTTAGAAGCATTTGGATTGACCCCA-----AGAGA 4137  
 QY 1709 LeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGlnGluAlaAspLysHisGly 1728  
 Db 4138 GCTCATATTGTATTAATAATCTTTTGAATTTTGAACCCCAAGCTGAAACAAAAA 4197  
 QY 1729 IleHisAspProHisValArgHisThrTyrLysSerAsnCysLeuProLeuArgPheTyr 1748  
 Db 4198 ATCACAGATCCTGACGTGATACATATTGGAACAAACAGCCCTTCCTGCTGCTG 4257  
 QY 1749 ValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp 1768  
 Db 4258 GTAAACATCTCGAAAGAACCTCGATGTCTTGAACATTAAGAGACACACATATAGAC 4317  
 QY 1769 AlaCysLeuSerValAlaAlaGlnThrPheMetAspSerCysSerThrIleSerGluHisArg 1788  
 Db 4318 GGCTGTTGTGAGATGATGCCAGGACATTCATGATCATTTCTCTCACAGAGCAACAA 4377  
 QY 1789 LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808  
 Db 4378 CTAGGAGAGAGAACCAACATTAATACCTTCTATGCCAAGATATCCCACTACAAA 4437  
 QY 1809 AsnTyrValGluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAsp 1828  
 Db 4438 GAAGAATGAATTTTACTGAGATCTGAATCTAAGAAACATAAATGAATTAATGAAGAGTG 4497  
 QY 1829 MetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetLysGlnLysPheAsnThrMetSer 1848  
 Db 4498 ATGAGAGATTTTAACTGAGATCTGAATCTAAGAAACATAAATGAATTAATGAAGAGTG 4557  
 QY 1849 AlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGlnGluIleLeuGlyProLeu 1868  
 Db 4558 GCCTTGACAGAAATTTCAATATCATGCTAAATATTTGATGATGATTTCAATTAACCTA 4617  
 QY 1869 AspHisAsp-----AspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1883  
 Db 4618 GAAAGAGAACAGAGGCTGTGAAGAAAGCTGAGAAACAACTCTTGATGATTAAGATC 4671

## RESULT 8

US-09-023-655-603

; Sequence 603; Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:



FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4626 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-306-691B-22

Alignment Scores:  
Pred. No.: 2,866-57 Length: 4626  
Score: 629.50 Matches: 282  
Percent Similarity: 35.47% Conservative: 204  
Best Local Similarity: 20.58% Mismatches: 409  
Query Match: 6,308 Indels: 475  
DB: 1 Gaps: 59

US-09-964-956-13 (1-1896) x US-09-306-691B-22 (1-4626)

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QY 62 HisIleTyrLeuG1ValAlaValAsnArgIleTyrLysLeuSer--SerAspLeuLysVal 80
DB 375 CACATTTTCCTTGGTCCCTAAGCTTATGTTTAAAGAGAAAGACCTTCAGAG 434
QY 81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIle 100
DB 435 GTTGCTGAGTACAGAGCTGGCCCTGTGTGGAACCCAGATTGTTCCTCA----- 485
QY 101 ValGlnThrCysAsnGlnProLeuThrThr-----AspAsnValAsn 115
DB 486 TGTCTAGAGCTGACGAGCAAGCCATTATTCAGAGGCTTTGGAAAGATACATCAAC 545
QY 116 LysMetLeuLeuIleAsp--TyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyr 134
DB 546 ATGGCTCTAGTGTGACACACTACTATGATGATCAACTCATTAAGTGTGGCGCTCAAC 605
QY 135 GlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProGlyHis 154
DB 606 AGAGGAGCTGCCAG-----CGACATGCTTT-----CCCCACAT 641
QY 155 LysLysGluHisTyrLeuSerGlyValAsn-----GluSer 166
DB 642 CATACTGCTGACATACATCGAGGCTTCATGATTCCTCCCAAGATAGAGAGCC 701
QY 167 GlySerValPheGlyValIleValSer-----TyrSerAsnLeuAsp 180
DB 702 AGCCAGCTGCTGACTGTGTGTGAGCGCCCTGGAGCCAAAGTCTTTCATCTTAAAG 761
QY 181 AspLys-----LeuPheIleAlaThrAlaValAspGlyLysProGluTyrPhePro 197
DB 762 GACCGGTTCATCACTCTTTTGAAGCAATACCAATAATCT--TCTTATTTCCCA 815
QY 198 -----ThrLysSerArgLysLeuThrLysAsnSerGluAlaAspGly 212
DB 816 GATCATCCATTCGATTCGATATCAGAGAGCTTAAGAGAAACGAAA-----GATGGT 869
QY 213 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp 232
DB 870 ---TTATGTTTTGAAGCAAGCTTCATTT----- 899
QY 233 ThrPheThrIleLeuProAspPhe-----AspIleTyrTyrValTyrGlyPhe 248
DB 900 -----GATGTTTACCTGAGTTCAAGAGATTCCTTACCCTTAAGATATTCATCCCTTT 953
QY 249 SerSerGlyAsnAspValTyrPheLeuThrLeuGlnProGluMetValSerProGly 268
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DB 954 GAAAGCAACAATTATTAATTACTTGTAGCGTCCAAAGGAA----- 995
QY 269 SerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThr 288
DB 996 ---ACTGTAGATCTCAAGACTTTTCAACAGAAATATACAGTTCTGTTCATTAACCTCT 1052
QY 289 AlaPheAsnSerTyrValGluValProIleGlyCys-----Glu 301
DB 1053 GSATTTGATTTCTTACATGGAAGAGCTCTGAGATGTATTTCTACAGAAAAAGAAAAAAG 1112
QY 302 ArgSerGlyValGlu-----TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGly 319
DB 1113 AGATCCACAAAGAGAGAGAGTTTAATATTAATTCAAGCTGCGGTATGTCCAGCAAGCCTGG 1172
QY 320 AlaValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPhe 339
DB 1173 GCCCAGTTCCTTACACAAATAGAGCCAGCTCAATGATGATCTTTTCGGGGCTTTC 1232
QY 340 SerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIle 359
DB 1233 GCACAAAGCAAGCCAGATTTCTGCCGAACCAATGATCGATCTGCTGATTCCTCT 1292
QY 360 LeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGly 379
DB 1293 ATCAATATGTCAACGACTTCTTCAACAG----- 1322
QY 380 ThrLeuAspLeuAlaTyrLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr 399
DB 1322 ----- 1322
QY 400 IleAspAsnAspPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal 419
DB 1322 ----- 1322
QY 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 439
DB 1323 -----ATCGTC 1328
QY 440 TyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArg 459
DB 1329 AACCAAAACATATG----- 1343
QY 460 ValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValAlaAspProGly 479
DB 1344 -----AATGCTCCAGCAT----- 1358
QY 480 ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499
DB 1359 -----TTTTCGGAACCAATCATGAG----- 1379
QY 500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519
DB 1379 ----- 1379
QY 520 LeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLys 539
DB 1380 -----CACTGC-----TTTAATAGCACTTTCAGAAAT 1409
QY 540 GluArg-----CysGluArgSerLysGluProArgArg-----PheAlaSerGluMetLys 556
DB 1410 TCATCAGCGCTGTGAAGCGCCCTGATGAATATCGAAGAGAGTTTCCACAGCTTTCGAG 1469
QY 557 GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeu 576
DB 1470 CGCGCTT-----GACTTATTCATGTGGTCAATTCACAGCAAGCT 1505
QY 577 LeuVal-----LeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594
DB 1506 CTCTTAACATCTATATCACTTCATTAAGAGAGACTC-----ACC 1547
QY 595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614
DB 1548 ATACCTAATCTTGGACATCAGAGAGGCGCTTCATGACAGGTGTGGTTCTCATCAGGA 1607
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Cy	615	ProkhlalAlaySGluValProArgGlelleThrgluenglyAspHisHlValValGln	634
Db	1608	CCATCAACCCCTCATGTGAATTTCCTCGT-----GACTCCATCAGTG---	1652
Cy	635	LeuGlInleuYsserLYsgluThrGlyMetThrPheAlaserThrserPheValPheTYr	654
Db	1652	-----	1652
Cy	655	AasnCysserValHisAasnSerCysIeuSerCysValGluSerProTYrArgCYshHsrtp	674
Db	1653	-----TTCTCCA-----	1658
Cy	675	CysLYSTYrArgHisValCysThrHisAspProLYstrCYsserPheGlnGLYrArg	694
Db	1658	-----	1658
Cy	695	VallyslauProGluAspCyseProGluInleuKrtgValAspLYslleuValProval	714
Db	1658	-----	1658
Cy	715	GluValIlleLYpProIleThrlleuYsalAlasAnleuProGlnProGlnserGlyGln	734
Db	1659	GAAGTGATGTGGAGACATACATA-----AACCAA	1688
Cy	735	ArgGIYTYrGLucYsIIleuAnslleglnglyserGluGlnArGVALProAlaleuArg	754
Db	1669	AATGGCTACACACTGGTTATCACT-----	1712
Cy	755	PheAnserSerSerValGlnCysGlnAasnThrserTYserTYrGluGlyMetGluile	774
Db	1713	-----GGAGAAGAATC	1724
Cy	775	AsnleuLepProVALGluIeuthrValValTrpangly-----HisPheasn	790
Db	1725	ACGAGAAATCCCCATTC-----AATGGCTTGGGCTGCAGACATTC--	1753
Cy	791	IleaPanProAlaglAsnLYslValHisleuTYrLYscysGlyAlametArggluSer	810
Db	1764	-----CAGTCC	1768
Cy	811	CysGlyLeuCYsLeuLYsalAspProAspPheAlaCYsGlyTYrCYeglnglyProgly	830
Db	1770	TGCAGTCATGCTCTCTGCCCCACCCTTGTTCAGTGGCTGGTGGCAC-----GAC	1823
Cy	831	GlnCYstHrleuArgGlnHiscYseProAlaglngInsrglnTrpLeuGluIreusergly	850
Db	1824	AATGTGGCAATCGGAGGAATGC-----CTGAGCCGG	1855
Cy	851	AlalySerLYs-----CysThrAsnProArgIlethrGluIleIleProvalThrgly	868
Db	1857	ACATGACATCAACAGATCTGTCTG---CTGCAATCTCAAGGTTTTCCCAATGTGTCA	1913
Cy	869	ProAcsgGluGlyGlyThrylsValhrllleaRgLygluAnslLeuGlyLeuGluPhearg	888
Db	1914	CCCCTTGAAAGGGACAAAGGTGCACATGTGGCTGGGACATTGGA-----TTTCGG	1966
Cy	889	-----AspIleAlaserHisValLYsValAlaglyValGluCYsserPro	903
Db	1968	AGGAATAATTAATTGATTTAAGAAAATAAGTAGTTCTCCTTGAAATAGAGCTGCACC	2027
Cy	904	LcuValAspGlyTYrIleProAlagluGlnIleValCYsGluMetGlyGluAlalyserPro	923
Db	2028	TTGACTTTAAGTAGACACGATGAATACATTGAATGACAGTTGGT-----CCT	2078
Cy	924	SerGlnHisAlaglyPheValGluIleCYsValAlaValCYsarGProGluPheMetala	943
Db	2079	GCCATGAATTAAGCATTTTC---AATATGTCCATAATTAATTTCAAATGGCCACGGGACAACA	2135
Cy	944	ArgserSerGlnleuTYrTYrPheMetThrleuThrleuSerAspLeuLYrProserArg	963
Db	2136	CATATCAAGTACATTCCTAT---GTGATCTCTGTAATATACAGATATTTTCGCCGAATATC	2192

QY 964 G1PromeSerSerGlyGlyThrGlnValThi1LeThG1yThrAsnLeuSna1aGlySer 963

Db 2193 GGTCTTAATGGCTGGTGGCACTTAACTACTTAACTGAAATTAACCTAAACAGTGGGAAT 2252

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QY 1004 ILeValCysAsnThrThrThrSerSerAspGluValLeuGlnMetLysValSerValGlnVal 1023

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QY 1024 AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlnSerProThrIleVal 1043

Db 2373 GACTTAACCCCAAC---CGAGAGACAAGCATCTTCAGTTACCGGTGAAGATCCCATTTGTAT 2429

QY 1044 ArgIleGlnProGlnTyrPheIleVal----- 1052

Db 2430 GAATTCATCCCAACCAAAATCTTTATATAGTACTGGGAAAGAACTCTCAACATGTGC 2489

QY 1053 -----SerGlyAsnThrProIleAlaValTArgIleThnHisLeu 1065

Db 2490 AGTTTCTATTTTGGCTTTGCCAGTGGGGAGGACATTAACAGTGTGGAAAAACCTG 2549

QY 1066 AspLeuIleGlnAsnProGln-----IleArgAlaLysHisGlyGlyLysGlnHisIle 1083

Db 2550 AATTCAGTATGATGTCGCCAGATGTCATTAATGTGCATAGACAGAGAAAGAACTTTACA 2609

QY 1084 AsnIleCysGlnValIleAsnAlaThnGlu---MetThrCysGlnAlaProAlaLeuAla 1102

Db 2610 GTGCAGATGTCAACATCGCTCTAATTCGAAGATAATCTGTTGTACACTCTTCCCTG-- 2666

QY 1103 LeuGlyProAspHisGlnSerAspLeuThrGlnArgProGlnGlnPheIleLeu 1122

Db 2667 -----CAACAGCGAATGTGCAACTCCCCCTGAAAAACCAAGCTTT--TTCAATGTTA 2717

QY 1123 AspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 1142

Db 2718 GATGGAGATCCTTTCCAAATACTTT-----GATCTCATTTATGTACATAATCCT 2765

QY 1143 ValPheGlnAlaPheGlyProSerGlyIleLeuGlnLeuLysProGlyThrProIleIle 1162

Db 2766 GTGTTTAAGCTTTTGAAGAACCCAGCATGATATCTCAATGGGCAATGATAATGTACGGA 2825

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Db 2826 ATTAAGGAAATGATATTGACCCCGAAGCAAGTAAAGTGAAG----- 2870

QY 1183 ValLeuValGlyGlnLysProCys---ThrValThrValSerAspValGlnLeuLys 1201

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QY 1202 GluSerProAsn---LeuIleGlyArgHisLysValMetAlaArgValGlyGlyMetGlu 1220

Db 2931 ACGGTCCCAATGACTGTGTAATTTGAACGCAGCTA-----AATATGAG 2978

QY 1221 TyrSerPro-----GlyMetValTyrIleAlaProAspSerPro 1233

Db 2979 TGGAAAGCAAGATTTCTTCAACCGCTCTGGAAAGAAATATAGTTCAACAGATCAGAAAT 3038

QY 1234 LeuSer-----LeuProAlaIleValSerIleAlaValAlaGlyGlyLeuLeuIleIle 1251

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QY 1252 PheIleValAlaValIleuIleAlaTyrLysArgLysSerArgGlnSerAspLeuThrLeu 1271

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QY 1272 LysArgLeuGlnMetGlnMetAspAsnLeuGlnSerArgValAlaLeuGlnCysLysGln 1291

Db 3159 TACGATGGAAGATACACATCCCTCATTTGGATAGCTTGGTAAGTGCAGGAAGTGAAGC 3218

QY 1292 AlaPheAlaGlnLeuGlnThrAspIleHisGlnLeuThrSerAspLeuAspGlyAlaGly 1311

Db 3219 CCAACTACAGAAAGGTTTCAAT----- 3242  
Qy 1312 IleProPheLeuAspTyrArgThrTyrThreMetArgValLeuPheProGlyIleGluAsp 1331  
Db 3243 --GATCTGTAGTACCTACCGAGCTACTTTCCAGAAAGATCATCTTCAATTCATCTCAG 3299  
Qy 1332 HisProValLeuArgAspLeuGluValPro 1341  
Db 3300 AACGTTATGCGCCAGCAAGTCAGATCTCT 3329  
RESULT 10  
PCT-US93-06251-27  
Sequence 27, Application PC/TUS9306251  
GENERAL INFORMATION:  
APPLICANT: Wickstrom, Eric and Rife, Jason P.  
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
NUMBER OF SEQUENCES: 93  
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06251  
FILING DATE: 19930630  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Digilio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 8586  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ. ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4626 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-27  
Alignment Scores:  
Pred. No.: 2,866-57 Length: 4626  
Score: 629.50 Matches: 282  
Percent Similarity: 35.47% Conservative: 204  
Best Local Similarity: 20.58% Mismatches: 409  
Query Match: 6.30% Indels: 475  
Gaps: 59  
US-09-964-956-13 (1-1896) x PCT-US93-06251-27 (1-4626)  
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Db 375 CACATTTCCTGCTGCGCCACTACCTACATTATGTTTAAATGAGGAACCTTCAGAG 434  
Qy 81 LeuValThrHisGluThrGlyProAspGluAspAsnProIysCysTyrProProArgIle 100  
Db 435 GTTGCTGAGTACAGAGCTGGCTGTGCTGGAACACCCAGATGTGTTCCA----- 485  
Qy 101 ValGlnThrCysAsnGluProLeuThrThr-----AsnAsnValAsn 115  
Db 486 TGTGAGACTGCGACGAGCAAGCCATTATATCAGAGGTGTTGAAAGATTAATCAATCAAC 545

Qy 116 LysMetLeuLeuIleAsp---TyrIysGluAsnArgLeuIleAlaCysGlySerLeuTyr 134  
Db 546 ATGGCTCTGATGTTGTCAGACACCTACTATGATGATCAATCATAGCTGTGCGAGCTCAAC 605  
Qy 135 GlnGlyIleCysAlaLeuLeuLeuArgLeuGluAspLeuPheLeuGluValProTyrHis 154  
Db 606 AGAGGAGACCTGCCAG-----CGACATGCTCTT-----CCCAAT 641  
Qy 155 LysGluGluHisTyrLeuSerGlyValAsn-----GluSer 166  
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Qy 167 GlySerValPheGlyValIleValSer-----TyrSerAsnLeuAsp 180  
Db 702 AGCCAGTGTCTGACTGTGTGTGAGCGCCCTGGAGCCAAAGTCTTTCATCTGTAAAG 761  
Qy 181 AspLys-----LeuPheIleAlaThrAlaValAspGlyLysProGluTyrPhePro 197  
Db 762 GACCGTTATCATCACTCTTCTTGAGCAATACCATTAATCT-----TCTATTTCACA 815  
Qy 198 -----ThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGly 212  
Db 816 GATCATCATTCATTCATTCATATCAGAGAGAGCTTAAAGAAACGAA-----GATGCT 869  
Qy 213 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp 232  
Db 870 ---TTATGTTTTCAGCGACAGCTCTTACATT----- 899  
Qy 233 ThrPheThrIleLeuProAspPhe-----AspIleTyrTyrValTyrGlyPhe 248  
Db 900 -----GATGTTTACCTGAGTTCAGAGATTTCTTACCCATTAAATGATGCTATGCTT 953  
Qy 249 SerSerGlyAsnPheValTyrPheLeuThrLeuGluProGluMetValSerProGly 268  
Db 954 GAAAGCAACAAATTTTATTAATCTTTCAGCGTCAAGGAA----- 995  
Qy 269 SerThrThrIysGluGluValTyrThrSerLysLeuValArgLeuCysIysGluAspThr 288  
Db 996 ---ACTCTAATGCTCAGACTTTCACACAAATATATCAGGTTGTTCCATTAATCTCT 1052  
Qy 289 AlaPheAsnSerTyrValGluValProIleGlyCys-----Glu 301  
Db 1053 GGAATTGATTCCTACATGAGAAATGCTCTGAGCTGATTTCTCACAGAAAAAGAAAAAG 1112  
Qy 302 ArgSerGlyValGlu-----TyrArgLeuLeuGluAlaAlaTyrLeuSerLysAlaGly 319  
Db 1113 AGATCCCAAGAAAGAAAGAGTTTATATATCTTCAGGCTGCGTATGTCAGCAAGCTGGG 1172  
Qy 320 AlaValLeuGluValArgThrLeuGluValHisProAspAspAspLeuLeuPheThrValPhe 339  
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Qy 380 ThrLeuAspLeuAlaThrLeuLysValIleAspIleProCysSerSerAlaLeuThr 399  
Db 1322 ----- 1322  
Qy 400 IleAspAsnAspPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal 419  
Db 1322 ----- 1322  
Qy 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 439  
Db 1323 -----ATGCTC 1328

QY 440 TyrIysAsnHisSerLeuAlaPheValGlyThrIysSerGlyLysLeuLysIleArg 459  
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 1344 -----AGATGCTCCAGCAT----- 1358  
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 1359 -----TTTACGAGCCCAATCATGAG----- 1379  
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 QY 577 LeuVal-----LeuGlnThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594  
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 1608 CCATCAACCCCTCATGTGAATTTCTCGT-----GACTCCCATCAAGT----- 1652  
 QY 635 LeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654  
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 1652 ----- 1652  
 QY 655 AsnCysSerValHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTyr 674  
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 1653 -----TCTCA----- 1658  
 QY 675 CysLeuTyrArgHisValCysThrHisAspProLysThrCysSerPheGlnGluLysArg 694  
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 QY 755 PheAsnSerSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIle 774  
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 1713 -----GGGAAGAAAGATC 1724  
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Db 1764 ----- 1769  
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 QY 831 GlnCysThrLeuArgGlnHisCysProAlaGlnGlnIserGlnThrLeuGlnLeuSerGly 850  
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 1824 AATGTGTGGCATCGAGAAATGC-----CTGAGCGG 1856  
 QY 851 AlaLysSerLys-----CysThrAsnProArgIleThrGluIleIleProValThrGly 868  
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 1857 ACATGACATCAAGATCTGTCTG-----CTGCATATTCAGAGTTTCCCAATAGTGA 1913  
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 1914 CCCCTTGAAGAGAGGACAAGGCTGACCATATGTGGCTGGACTTTGA-----TTTCGG 1967  
 QY 889 -----AspIleAlaSerHisValLysValAlaGlyValGluCysSerPro 903  
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 1968 AGGAATATATTAATTTGATTTAAAGAAACTAGAGTTCTCTTGGAATAGAGCTGCACC 2027  
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 2028 TTGACTTAAGTAGAGAGCAGATGATATCATGAAATGACAGATTGCT-----CCT 2078  
 QY 924 SerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAla 943  
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 2136 CAATACAGTACATTCCTCAT-----GTGATCTCGTAATTAACAAGTATTTGCGCGAATAC 2192  
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 2373 GACTTAGCCAAC---CGAGAGACAGAGATTTCAATTACCGGTGAAGATCCCATTTGCTAT 2429  
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 QY 1053 -----SerGlyAsnThrProIleAlaValTyrGlyThrHisLeu 1065  
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 QY 1084 AsnIleCysGluValLeuAsnAlaThrGlu--MetThrCysGlnAlaProAlaLeuVal 1102  
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 2610 GTGGCATGTCAACATGCCCTTATATCAAGATATATGTTGACACTCTTCCCTG--- 2666  
 QY 1103 LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeu 1122  
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 2667 -----CAACAGCTGAATCTGCAACTCCCTGAAACCAAAACCTTT---TTCAATGTA 2717  
 QY 1123 AspAsnValGlnIserLeuLeuIleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 1142



Db 2718 GATGGGATCTTTCCAAATCTT-----GATCTCATTTATGATCAATCTCT 2765  
 QY 1143 ValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle 1162  
 Db 2766 GTGTTTAAGCTTTTGAAGAACCGATGATGATCTCAATGGGCAATGAAATGATACGAA 2825  
 QY 1163 LeuLysGlyLysAsnLeuIleProProValAlaGlyLysValLysLeuAsnIleThr 1182  
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 QY 1183 ValLeuValGlyLysProCys---ThrValThrValSerAspValGlnLeuLysCys 1201  
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 QY 1202 GluSerProAsn---LeuIleGlyArgHisLysValMetAlaArgValGlyLysMetGlu 1220  
 Db 2931 ACGGTCCCAATGACCTGCTGAATTTGAACAGCAGCTA-----AATATAGAG 2978  
 QY 1221 TyrSerPro-----GlyMetValIleAlaIleAlaProAspSerPro 1233  
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 QY 1234 LeuSer-----LeuProAlaIleValSerIleAlaValAlaGlyLysLeuLeuIle 1251  
 Db 3039 TTTCACAGATTGATTCGTGGTGTGTCTCATATCAACAGCAGCTGTATTACTTCTGGG 3098  
 QY 1252 PheIleValAlaValLeuIleAlaTyrLysArgLysSerArgLysSerAspLeuThrLeu 1271  
 Db 3099 TTTTTCCTGCTGGCTGAAGAAAGAAAGCAAAATTAAGATCTGGCAGAGTAATTTGTTGCC 3158  
 QY 1272 LysArgLysGluMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGlu 1291  
 Db 3159 TACGATGCAAGATGACACACCTCCATTTGGATAGAGCTGTGAAGCCCGAAGGTAGAGC 3218  
 QY 1292 AlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly 1311  
 Db 3219 CCACTACAGAAATGTTTCAAAAT----- 3242  
 QY 1312 IleProPheLeuAspTyrArgThrTyrThrMetArgValLeuPheProGlyIleGluAsp 1331  
 Db 3243 ---GAATCTGATGACTACCGAGCTACTTTCCAGAAGATCACTTCCATTCATCTCAG 3299  
 QY 1332 HisProValLeuArgAspLeuGluValPro 1341  
 Db 3300 AACGGTTTCATGCCGACAAAGTGCAGTATCTCT 3329  
 RESULT 11  
 US-09-300-958A-24  
 ; Sequence 24, Application US/09300958A  
 ; Patent No. 6495319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCelland, Michael  
 ; APPLICANT: Welsh, John  
 ; APPLICANT: Trentle, Thomas  
 ; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
 ; FILE REFERENCE: P-PH 3457  
 ; CURRENT APPLICATION NUMBER: US/09/300,958A  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: 60/083,331  
 ; PRIOR FILING DATE: 1998-04-27  
 ; PRIOR APPLICATION NUMBER: 60/098,070  
 ; PRIOR FILING DATE: 1998-08-27  
 ; PRIOR APPLICATION NUMBER: 60/118,624  
 ; PRIOR FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 85  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 24  
 ; LENGTH: 2433  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-300-958A-24

Alignment Scores:  
 Pred. No.: 3,226-24 Length: 2433  
 Score: 323.00 Matches: 184  
 Percent Similarity: 36.19% Conservative: 128  
 Best Local Similarity: 21.35% Mismatches: 309  
 Query Match: 3.23% Indels: 241  
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 US-09-964-956-13 (1-1896) x US-09-300-958A-24 (1-2433)  
 QY 36 LysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuVal 55  
 Db 1 GAAGAAAGGCTGATTAGAAATTTGAAGCTGAAACATCTCCAACTACAGCGCCCTTGTG 60  
 QY 56 ValAspGluArgThrGlyHisIleTyrLeuGluValAlaAsnArgIleTyrLysLeuSer 75  
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 QY 76 SerAspLeuLysValLeuValThrHisGlu-----ThrGlyProAspGlu 90  
 Db 121 AGCAACTCAGCTTCTTCCAGCGGGAGTACCAAGACTACTGTGAGTGCAGATGCT 180  
 QY 91 AspAsnProLysCysIleTyrProProArgIleValGlnThrCysAsn-----Glu 106  
 Db 181 GACAGGAG-----CAGCATGACAGCTTCAAGGCAAGAC 216  
 QY 107 ProLeuThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArg 126  
 Db 217 CCAAGCGAGCTGTGAAGAACTACATCAAGATCTCTCTG---CCACTCAACAGCAGCCAC 273  
 QY 127 LeuIleAlaCysGly---SerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAsp 145  
 Db 274 CTGCTCAGCTGTGGCAGCGGCCCTTACAGCCCTGTGTGCTTACATTACATAGAGAGC 333  
 QY 146 LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGlu 165  
 Db 334 ---TTTACTTTAGCCCA-----GATGAG 354  
 QY 166 SerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp----- 180  
 Db 355 GCCGTAATGTCAAT-----CTGAGAGATGCGAAGGCTCAT 390  
 QY 181 ---AspLysLeuPheIleAlaThrAla-----ValAspGlyLysProGluTyr 195  
 Db 391 TGTCCCTTTGACCCCACTTCAAGTCCAGGCTCTGTGTGTGATGTGT-----GAGCTG 444  
 QY 196 Phe-----ProThrIleSerSerArgLysLeu 204  
 Db 445 TACACGTGAACAGTCACTAGCTTCCAGGAAACGACCCAGCTATTTCCCGAGCGCAGAGT 504  
 QY 205 ThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAla 224  
 Db 505 TCCGCCCCCAAGACTGAGACTCTCCCACTGCTGCTACAAACCTCGCTTTGTGGCC 564  
 QY 225 SerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyr 244  
 Db 565 TCGGCTACGTCCTCCGAGAGCTGTGGGAGCCCATAGTATGATAGATAGATCACTACTTC 624  
 QY 245 ValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetVal 264  
 Db 625 TTCTTCAGCAGACGGGCGCAGAGTTTGACTCTT----- 660  
 QY 265 SerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCys 284  
 Db 661 -----GAGAACACCATGCTGCCAGATGGCCAGTCTGT 696  
 QY 285 LysGluAspThrAla-----PheAsnSerTyrValGluVal 296  
 Db 697 AAGGCGCATGAGGGTGAAGAGCGGGTGTGCAGACAGCTGAGCTCTTCTTCAAGGCT 756  
 QY 297 ProIleGlyCysGluArg-----SerGlyValGluTyrArgLeuLeuGlnAlaIleTyr 314  
 Db 757 CAGCTCCTGTCTCCCGGCGCTGATGATGATGCTTCCCTTAAACGTCACAGATGTCTTC 816

QY 315 LeuSerIysAlaGlyAlaValLeuGlyValThrLeuGlyValHisProAspAsp----- 332  
 DB 817 -----ACCTGAAACCCCAACCTCCAGGATTGGCGC 846  
 QY 333 ---AspLeuLeuPheThrValPheSerIysGlyIleuValGlyMetIysSerLeuAsp 351  
 DB 847 AAGACCCCTTTCTATGGGGCTCTTACCTCCAGTGGCAGCA-----GGACCAACAGAA 900  
 QY 352 GluSerAlaLeuCysIlePheIleLeuIysGlnIleAsnAspArgIleIysGluArgLeu 371  
 DB 901 GGCTCGGCATCTGGCTTCCACCATG-----AATGAT---GGCAAGAGGCTTT 948  
 QY 372 GlnSerCysTyrArgGlyGluGlyThrIleuAspLeuAlaTyr---LeuIysValIlyAsp 390  
 DB 949 GAGGCGCTGTACAAAGAAAGTAAACAGAGACACAGCATGGTATTACCGAACCACAG 1008  
 QY 391 IleProCysSerSerAlaLeuLeuThrIleAspAsnAspPheCysGlyLeuAspMetAsn 410  
 DB 1009 GTGCCCAACACCGCGCGGAGCGTGCATTACCAACAGTGCCTGGGAAACGAGATCAAC 1068  
 QY 411 AlaProLeuGlyValSerAsp----- 417  
 DB 1069 TGGTCCCTGGACCTCCAGACCGAGTGTAACTTCTCAAGATCACTTCTTATGAGT 1128  
 QY 418 ---MetValArgGlyIleProValPheThrGluAspArgAspMetThrSerValIle 436  
 DB 1129 GGGCAGGTCCGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1188  
 QY 437 AlaTyr-----ValTyrIysAsnHisSerLeuAlaPheValGlyThrIlySer 452  
 DB 1189 GTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
 QY 453 GlyIysLeuIysIleArgValAspGlyProArgGlyAsnAlaLeuGlyTyrGluThr 472  
 DB 1249 GGGCGCTCAGCAAAAGACATGACCTGAGCTCCAGATCCAGATCCAGATCCAGATCCAGAT 1302  
 QY 473 ValGlnValAlaAspProGlyProValIleuArgAspMetAlaPheSerIysAspHisGlu 492  
 DB 1303 CTGCAGATCTTCTCCCAAGACAGCTGTCAGAACTCTGCTTGGACAGCATGGGGA 1362  
 QY 493 GlnLeuTyrIleMetSerGlnArgGlnLeuThrArgValProValGluSerCysGlyGln 512  
 DB 1363 CTGTTGATGCTCTCTCCATTCCGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1422  
 QY 513 TyrGlnSerCysGlyGlnCysAlaLeuIysSerGlyAspProHisCysGlyTyr----- 529  
 DB 1423 TACCAACTGTGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482  
 QY 530 ---CysValLeuHisAsnThr----- 535  
 DB 1483 GCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542  
 QY 536 -----CysThrArgIysGlnArgCysGlyIysSerIysGlnProArgIysPheAla 552  
 DB 1543 ATTGAGGGTGCAGTGTCAAGAACTCTGCAAGAACTCTGCAAGAACTCTGCAAGAACTCTGCT 1602  
 QY 553 SerGluMetIysGlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGln 572  
 DB 1603 GTGCCAGGTAAAGCATGTAACAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 1662  
 QY 573 TyrAsnValLeuLeuValLeuGluThr-----TyrAsnValProGluLeuSer 588  
 DB 1663 TGGCCACTGCTCTCAAACTGGGCACTGGCTCTGGGTCACAAATGAGAGCCCACTCAT 1722  
 QY 589 AlaGlyValAsnCysThrPheGluAspLeuSerGluMetAspGlyIysValValGlyAsn 606  
 DB 1723 GCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1776  
 QY 609 Gln-----IleGlnCys----- 612  
 DB 1777 CAGCAGAGTTTGGGGGTGTTCCAGTGTGTGTCATGAGAGAGATTCACAGAGCTGTG 1836

QY 613 -----TyrSerProAlaAlaIysGlu----- 619  
 DB 1837 GCCAGCTACTGCCCCAGAGGTGATGAGAGAGGGGTATGACCAAAAGACAGCGTAT 1896  
 QY 620 ---ValProArgIleIle-ThrGluAsnGlyAspHisIleValValGlnLeuGlnLeu 638  
 DB 1897 GGNACCCAGCATATTATCAACA-----CATCAGAGTGAAGTGCACCGGCTGGT 1944  
 QY 638 SerSerGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerVal 658  
 DB 1945 GGCAGGACAGCTGGGGTGGGACAGTCTTACGATGGAATGATTCCTGGATGTGCTACT 2004  
 QY 658 HisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTyrCysIysTyr 678  
 DB 2005 C-----TGTTGTGTGTTGCTA-----TGATGC----- 2026  
 QY 678 GlnIysValCysThrHisAspProIysThrCysSerPheGlnGlu----- 692  
 DB 2027 -----TTTGT-----TTCTGTTCTTCTTACCCGATCGGATGGCATG 2067  
 QY 693 -----GlyArgValIysLeuProGluAspCysProGlnLeu----- 704  
 DB 2068 AAACCTTCTTAAGAGGGCGAGGTGTCACAGTGGACCCCAAGACTGACCTATAGT 2127  
 QY 705 -----LeuArgValAspIysIleLeuValProValGluValIleIysProIleThrIle 722  
 DB 2128 CTACCACTGAGACCGGACCGGCTGATGTTGGCGCTCTTACGACCCCACTTGAACAC 2187  
 QY 722 uIysAlaIysAsnLeu-----ProGln---ProGlnSerGly-----G1 734  
 DB 2188 CAGGCTTACAGGCTCTGTGCGATGAGCTCCAGAGGCCAGAGTCTTCACTGATCAAGAG 2247  
 QY 734 nArgIlyTyr-----GluCysIleLeuAsnIleGlnIys 746  
 DB 2248 AAGAGGCCACTGATGATCCAGAGACAGCTTGTGAGAGTGTCTCCGTGTCCCGGCC 2307  
 QY 746 rGlu 747  
 DB 2308 CGAG 2311  
 DB 2308 CGAG 2311  
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 US-09-077-940A-3  
 : Sequence 3, Application US/09077940A  
 : Patent No. 6576441  
 : GENERAL INFORMATION:  
 : APPLICANT: KIMURA, Toru et al.  
 : TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME  
 : FILE REFERENCE: 0020-4426P  
 : CURRENT APPLICATION NUMBER: US/09/077,940A  
 : NUMBER OF SEQ ID NOS: 20  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 3  
 : LENGTH: 3524  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: 5'UTR  
 : LOCATION: (1)..(38)  
 : OTHER INFORMATION:  
 : NAME/KEY: 3'UTR  
 : LOCATION: (2706)..(3524)  
 : OTHER INFORMATION:  
 : NAME/KEY: CDS  
 : LOCATION: (39)..(2702)  
 : OTHER INFORMATION:  
 : US-09-077-940A-3  
 Alignment Scores:  
 Pred. No.: 2,46e-17 Length: 3524  
 Score: 263.00 Matches: 144  
 Percent Similarity: 36.91% Conservative: 90  
 Best Local Similarity: 22.71% Mismatches: 208

Query Match: 2.63% Indels: 192  
 DB: 4 Gaps: 34  
 US-09-964-956-13 (1-1896) x US-09-077-940A-3 (1-3524)

QY 11 LeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeuLeuThrArgGlnPro 30  
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 DB 75 CTGCTGCTCTGCTGCTACTGAGG---GGCGCCACGCGCTCTTCTTCTGAGAACCG 131  
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QY 31 AlaProLeuSerGlnGlySerPheValThrPhe----- 43  
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 DB 132 CCGCCCTTACGCTGCGCCCGACGACCTACCTAACCACTCCGCTGTTGTGGCGAC 191  
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QY 44 -----ArgGlyGlnProAlaGlnGlyPheAsnHisLeuValValAsp----- 57  
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 DB 192 GGGCGCGGACGCGTACCCCGCAGAGGTGTCAGACCTCAACATCCAGAGGAGCTTG 251  
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QY 58 -----GlnArgThrGlyHisIleTyrLeuGlyValAlaAsnArgIleTyrIleLeu--- 74  
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 DB 252 CCGGTCAACAGAGC-----CTGTCATTGGGAGACAGGACCACTTACCGCGTAGAG 305  
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QY 75 -----SerSerAspLeuLysVal-----LeuValThrHisGlnThrGly 87  
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 DB 306 CTGAGAGCCCCCAGCTCAGAGCTGCGGTACAGAGAGAGTGAAGCTGAGAGATAC 365  
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QY 88 ProAspGlnAspAsnProLysCysTyrProProArgIleValGlnThrCysAsnGlnPro 107  
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 DB 366 CCCAGCCACATAAAGCTGTGTCGATGAGGCAACAGAGGCGAGGTGCGA----- 419  
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QY 108 LeuThrThrThrAsnValAlaAsnLysMetLeuLeuIleAspTyrIleGlnAsnArgLeu 127  
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 DB 420 -----AACTCGTAAAGGTGCTGCTCTCTCGGAC-----GAGTCCAGCTTC 461  
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QY 128 IleAlaCysGlySer---LeuTyrGlnGlyIleCysIleLeuLeuArgLeuGlnAspLeu 146  
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 DB 462 TTGTGTGGCGGTCCAAAGCCTTCAACCGGTGTGGCCCACTACAGCATAGACCCCTG 521  
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QY 147 PheIleLeuGlnGlyLeu-----ProPheHisLysIleGlnHis 158  
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 DB 522 CAGCCCGTCGAGCAACATCAGCGGTATGCGCCGCTGCGCCGTAACCCCAAG---CAC 578  
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QY 159 TyrLeuSerGlyValAlaGlnSerGlySerValPheGlyValIleValSer----- 175  
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QY 176 -----TyrSerAsnLeuAspAspLysLeuPheIleAlaIleVal 189  
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 DB 639 GCCATTGATGCTGCTCATCTACCGACGCTCGGGAGACG----- 677  
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QY 190 AspGlyLysProGlnIleTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGln 209  
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QY 210 AlaAspGlyMetPheAlaTyrValPheHisAspGlnPheValAlaSerMetIleLysIle 229  
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QY 230 ProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSer 249  
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QY 270 ThrThrLysGlnGlnValIleTyrThrSerLysLeuValArgLeuCysLysGlnAspThrAla 289  
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QY 290 -----PheAsnSerTyrValGlnValProIleGlyCys 300  
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 DB 855 GGCTCCCCCGCTGTGAGAGACAGTGAAGCTTCTCTGAAGGCGCGCTCAACTGC 914  
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QY 301 GlnArgSerGly-----ValGlnTyrArgLeuLeuGlnAlaAlaTyrLeuSerLys 317  
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 DB 915 TCTGTACCCGAGAGACTCCCATTTCTACTTCAAGCTGTGACAGGTCTTC----- 962  
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QY 318 AlaGlyAlaValLeuGlnGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThr 337  
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 DB 963 ACGGCGCTGGTCC-----AGCTCGAGGCGCGGCTC-----GTGCTCTGACC 1004  
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QY 338 ValPheSerLysGlnGlnLysArgLysMetLysSerLeuAspGlnSerAlaLeuCysIle 357  
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 DB 1005 GTTTTTC-----ACCCAGACAGACATCCCTGCTGCTGCTGCTGCTGCGCC 1052  
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QY 358 PheIleLeuLysGlnIleAsnAspArgIleLysGlnArgLeuGlnSerCysTyrArgGly 377  
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 DB 1053 TTTGACCTGACACAGGTGGAGCTGTGTTGAAGCGGC-----TTCCGAGAG 1100  
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QY 378 GlnGlyThrLeuAspLeuAlaTyrPheLysValLysAsp-----IlePro----- 392  
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 DB 1101 CAGAACTCCCGGAGTCCATCTGAGACCGCGGTCCGAGATCAGTGCCTCGACCCCGG 1160  
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QY 393 -----CysSerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsn 410  
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 DB 1161 CCGGAGTGTGCGGAGC-----CCCGGAGTACAGTACAT 1196  
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QY 411 Ala-----ProLeuGlyValSerAspMetValArgGlyIleProValPheThr 426  
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 DB 1197 GCTTCACAGCGCTTGGCGGATGATCATCTCACTTGTTCAGAACCCACCTCTGATGAC 1256  
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QY 427 GlnAsp-----ArgAspArg 431  
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 DB 1257 GAGGCGGTGCTGCTGAGCCATGAGCCCTGATCTGTGCGAGCCCTGATAGGACACAG 1316  
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QY 432 MetThrSerValIleAlaTyrVal-----TyrLysAsnHisSerLeuAlaPhe 447  
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 DB 1317 CTGACTCAGAGTGTGTCGACGTGAGACCGGCGCTGGGCAACAGACCGTGTCTTC 1376  
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QY 448 ValGlyThrLysSerGlyLysLeuLysIleArgVal-----Asp 461  
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QY 462 GlyProArgGlyAsnAlaLeuGlnTyrGlnThrValGlnValValAspPro----- 478  
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 DB 1437 GGGAGCTGTGGCTCAGGTCTTCTCTGAGGAGTTGAGACTTACCGGCGGAGAGGTGT 1496  
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QY 479 -----GlyProValLeuArgAspMetAlaPheSerLysAsp 490  
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QY 491 HisGlnGlnLeuTyrIleMetSerGlnArgGlnLeuThrArgValProValGlnSerCys 510  
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QY 511 GlyIleTyrGlnSerCys---GlyGluCysLeuGlySerGlyAspProHisCysGlyTyr 529  
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 DB 1617 CAGCAGTACTCGGGGTGATGAAGAATCTGTACGCACTAGAACCCCTACTGCGGGTGG 1676  
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QY 530 -----CysValLeuHisAsnThrCysThrArg 538  
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 DB 1677 GCCCGGACGCGCTCCTGATCTTCTCTCAGCCCGGAGACAG 1718  
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RESULT 13  
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 ; Sequence 1, Application US/09077940A  
 ; Patent No. 6576441  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMURA, Toru et al.  
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME  
 ; FILE REFERENCE: 0020-4426P  
 ; CURRENT APPLICATION NUMBER: US/09/077,940A  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1

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1 LENGTH: 3692
2
3 TYPE: DNA
4
5 ORGANISM: Rattus norvegicus
6
7 FEATURE:
8
9 NAME/KEY: 5'UTR
10
11 LOCATION: (1)..(18)
12
13 OTHER INFORMATION:
14
15 NAME/KEY: CDS
16
17 LOCATION: (19)..(2662)
18
19 OTHER INFORMATION:
20
21 NAME/KEY: 3'UTR
22
23 LOCATION: (2683)..(3653)
24
25 OTHER INFORMATION:
26
27 NAME/KEY: polyA site
28
29 LOCATION: (3554)..(3692)
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31 OTHER INFORMATION:
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33 OS-09-077-940A-1

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Alignment Scores:	
Pred. No.:	2,86e-15
Score:	141
Percent Similarity:	35.6%
Best Local Similarity:	22.17%
Query Match:	2.45%
DB:	4
	Gaps:
	34
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	Length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	303

US-09-964-956-13 (1-1896) X US-09-077-940A-1 (1-3692)

QY TrpDhp-----CysLeuIuseRhtLSleuMetValGly 19  
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QY MetGlySerSerThreuleuthrArgAlnProAlaProLeuSerGlnLysGlnAsger 39  
Db AGGATGAAACCATTGCGCTTTTCCAGATGAAACCACTCCACTCATGTGGGCTCCAGAGAC 141  
QY PheValThrPhe-----ArgGlyGluProAlaGlu 49  
Db TAAGTAGCACCACTAACCCCGTGTTCGAGGCAAGCGGCGCTGTGTCTGACCCCTGCAGAG 201  
QY GlyPheasnhtlsleuValasp-----GluArgThrGlyHisLysIer 64  
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QY LeuGlyValAlaValasnArgIleTyrlusleu-----SerSerAspleu 78  
Db ATCGGGGACAGAGAACAACCTGTACCAAGTACAGTACGCCATCCACATCCAGCGAGCTG 315  
QY LysVal-----LeuValThrHisglutThrArgLysProAlaArgLysAsnProLysCysTyx 96  
Db CGGATGACGCGAAGCTTACTGCGGCGCTCAACCCCAAGTAC----- 357  
QY ProBorArgIleValGlnThrCys-----AsnGluProLeuThrThrTrhAsn 112  
Db -----ATCATGTGTGTCCGATGAAAGCGCAACAAGGCTGAGTGTGGAGAC 405  
QY AsnValAsnLysMetLeuLeuIleAspTyrlysGluAsnArgLeuIleAlaCysGlySer 132  
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QY ---LeuTyrglnGlyllecyslysleuleuAlaGluLeuAlaProLeuPheLysLeuGlu 151  
Db AATGCAATTCATCCCATCTGTGCGAATTACAGTATGAGACACATCGACCTTTGGAGAC 519  
QY -----ProTyrHisLysLysGluHsrTyxLeuSerGlyVal 163  
Db AACATCAGTGTATGGCCCGCTGCCCTCAAGACCCCAAG-----CATGCCAATGTGCCCTC 576  
QY AsnGluSerGlySerValPheGlyValIleValser----- 175  
Db TTCCTCAATGGGATGCTCTTTCACAGGCCACAGTACTGACCTTCATGACATGACGCTGT 636  
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Db	637	ATTCACGTCGACCCCTGGGACCCGG-----	660
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Qy	215	AlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThrPhe	234
Db	682	-----CATGAC-----TCCAAAGGCTTAAAGACCA-----	708
Qy	235	ThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheVal	254
Db	709	-----TACTTGTGATCGCGGTGAGTGAGTGAGGGAAGGACACTC-----	744
Qy	255	TyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThrLysGluGln	274
Db	745	TACTCTCTCTCCGGGAGATGCGCATG-----GAGTTAACTATCTGAAAAAG	792
Qy	275	ValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla-----	289
Db	793	GTGGGTGGTGCCTCGGTGGCCCGGTGATGCAAGATAGTGTGGCGCGCTCCCAACGGCTG	852
Qy	290	-----PheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyx---	304
Db	853	CTGAGAAAGCAGTGGACTCTCTCTCTGTAAGGCCCGCGCTCAACTGCTCGTGGAGGAC	912
Qy	305	-----ValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyValAlaLeu	322
Db	913	TCACACTCTTCACTCAATGATCTAGTCAAGCTGTG-----ACTGGTGTGGTg--	957
Qy	323	GlyArgThrLeuGlyValHisProAspAspLeuPheThrValPheSerLysGly	342
Db	958	-----ACCTTGGCGGCGCTCA-----GGATCTCTGGCTGTTCTCA-----	996
Qy	343	GlnTyrArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGln	362
Db	997	-----ACTCTAGCAACAGCATCTCCGTGACGTGCTGTGCTTGACATGAAACCA	1055
Qy	363	IleAsnAspArgIleLysGluArgLeuInserCysTyrArgGlyGluGlyThrLeuAsp	382
Db	1051	GGGCTGCTGTGTTTGAAGCCGC-----TTCGGGAGCAGAAGTCACTGAG	1096
Qy	383	LeuAlaTyrPheLysValLysAsp-----IlePro-----CysSerSer	395
Db	1099	TCAACTCTGAGCCCGCTGCGTGAAGCACAAGTACCAACCGCCAGCCCGGGTGTGTGCA	1155
Qy	396	AlaLeuLeuThrIleAspAspAsnMetCysGlyLeuAspMetAsnAlaProLeuGlyVal	415
Db	1159	GGG-----CCCGTATGCAGTACACAGCTCAATGCCCTT	1194
Qy	416	SerAsp-----MetValArgGlyIlePro-----	423
Db	1195	CCTGACGAGATTCTCAACTTTGTAAAGCCCAACCACTGATGGAGCAAGCCGGTGCCTCC	1255
Qy	424	-----ValPheThrGluAspArgAspAspMetThrSerValIle	436
Db	1255	CTGGCCCACTGCCCTTGATGTGTGAAGAACTCTGATACGGCACCACTGACCCGAGTGGT	1311
Qy	437	AlaTyrVal-----TyrLysAsnHisSerLeuAlaPheValGlyThrLysSer	452
Db	1315	GTGGATGGGTGGTGCAGGCCCATGGGGCAATCAGACAATAGTCTTCTGGCTCTTAAGT	1377
Qy	453	GlyLysIleuLysLysIle-----ArgValAspGlyProArgGlyAsn	466
Db	1375	GGGACAGTCTCAAAATTCCTTGTGAAGCCCAATGCCAGTGTCTCAGGAGACACAGGGCCC	1433
Qy	467	AlaLeuGlnTyrGluThrValGlnValValAspPro-----	478
Db	1435	AGCATCTTTTGGAGGAGTTTGAGACCTACCGCCAGACAGGTGTGGACATCCACAGT	1499
Qy	479	-----GlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeu	494

Db 1495 GGTGTGAGTGGGACCAAGACTTCTGAGCTGAGTAGATGCTGCTCAGTGGCTG 1554  
QY 485 TyrIleMetSerGluArgGlnLeuThrArgValProValGluSerGlyGlnTyrGln 514  
Db 1555 CTGGACGCTTCCCGCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1614  
QY 515 SerGlySerGlyGlnLeuGlySerGlySerProHisCysGlyTyr 529  
Db 1615 GGTGTGAGTGGGACCAAGACTTCTGAGCTGAGTAGATGCTGCTCAGTGGCTG 1662

RESULT 14  
US-09-653-274-3  
Sequence 3, Application US/09653274  
Patent No. 6635742  
GENERAL INFORMATION:  
APPLICANT: Boyle, Bryan J  
APPLICANT: Yeung, George Y  
APPLICANT: Atteburn, Matthew C  
APPLICANT: Mize, Nancy K  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-like  
TITLE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: HVS-23  
CURRENT APPLICATION NUMBER: US/09/653,274  
CURRENT FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-10  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 3694  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (434)..  
US-09-653-274-3

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Pred. No.: 1,62e-13 Length: 3694  
Score: 228.50 Matches: 130  
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Best Local Similarity: 20.83% Mismatches: 227  
Query Match: 2.29% Indels: 167  
DB: 4 Gaps: 30

US-09-964-956-13 (1-1896) x US-09-653-274-3 (1-3694)

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Db 482 CAGTTAGGCGGACGCTTCTTCTGAGATGATGAAACCCCTTAAGTAAGTCTGACTATCAC 541  
QY 36 LysGlnArgSerSerHisValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuVal 55  
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QY 56 ValAsp-----GluArgThrGlyHisIleTyrLeuGlyAlaValAsnArg 70  
Db 602 CTGACATTTCACTGATGTTGAATAATTCAGACACACTTATATATGCTGGCAGGATCA 661  
QY 71 IleTyrIleLeuSerSerSerAspLeuValLeuValThrHisGlnThrGlyProAsp--- 89  
Db 662 GTTTATACAGTA-----AACTTAATGAATGCCCAAAACAGAAATTAATCCCAACAG 715  
QY 90 -----GluAspAsnProLeuCys---TyrProProArgIle 100  
Db 716 AAACGTGATGGGATCAAGACAAAGGATCGAATAAGTGTCTATGAAGGCAAGCAT 775

QY 101 ValGlnThrCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeu 120  
Db 776 AAGATGATGCCACAACTTATC-----AAAGATTTGTT 811  
QY 121 AspTyrIleGluAsnArgLeuIleAlaCysGly---SerLeuTyrGlnGlyIleCysLys 139  
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QY 140 LeuLeuArgLeuGluAspLeuPheLeuGlyGluProTyrHisLysLysGlnHisTyr 159  
Db 872 TACTACAGTTGATGATCTTGAATATGATGGGAAAGAA----- 910  
QY 160 LeuSerGlyVal-----AsnGluSerGlySerValPheGly 171  
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QY 192 LysProGluTyrPheProThrIleSerSerArgLysLeuThrIleAsnSerGluAlaAsp 211  
Db 1004 -----TTCTTGGCCAGCGATGCCGTTATTATTAAGCAATGGCTGAT 1045  
QY 212 GlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSer 231  
Db 1046 GGAATCGCCCTTGGCACATA-----AAATGATTCGAATGATTAAGAGCA--- 1096  
QY 232 AspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGly 251  
Db 1097 -----CACTTCTTCATGCCATGAAATATGGA 1123  
QY 252 AsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThr 271  
Db 1124 AACTAGCTATATTTCTTTCGAGAA-----ATCGCTCGAACAATTAATTTA 1174  
QY 272 LysGlnGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla----- 289  
Db 1175 GGCAGAGCTGTAT--TCCCGCGTGGCCCGCATATGTAACAAACAGATGGGTGCTCC 1231  
QY 290 -----PheAsnSerTyrValGluValProIleGlySerGluArg 302  
Db 1232 CAGCGGCTCTGGAGAAACATGAGCTTCACTTTCTAAAGGCTGGCTGAACCTTTCTGTC 1291  
QY 303 SerGly-----ValGluTyrArgLeuLeuGlnAlaIleTyrLeu 315  
Db 1292 CCTGAGATCCGTTTCTTCTACTTGTGATGTTCTGACGCTATACAGCATATATCAATC 1351  
QY 316 SerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeu 335  
Db 1352 AATGGCATCCCACTGTCGGG-----GTG 1378  
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Db 1379 TTTCACAG-----CACTCAATATCATCCCTGCTGCTGCTG 1417  
QY 356 CysIlePhe-----IleLeuLysGlnIleAsnAspArgIleLysGluArg--- 370  
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QY 371 -----LeuGlnSerCysTyrArgGlyValGluIleThrLeuAspLeuAlaTyr 385  
Db 1477 AACTCCAGATTTCTTTGAGACAGAGTTCCTCGAAGCAAGTGGCAAGCAAGGCTGG 1536  
QY 386 LeuLysValIleAspIleProCysSerSerAla-LeuLeuThrIleAsp-----AspAs 403  
Db 1537 CTGTTTGCAAAACACGCGCTTGGCGAAGCTTTAAACCTTCATCATTCCTCGGATGA 1596  
QY 403 nPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMet-----ValArgG 421  
Db 1597 AACTGTGTCATTCATCAATCTCATCCCTGATGGAATCTGCGCTTCCACCCATTTGCCGA 1656

QY 421 YLleProValPheThrGluAsp-----ArgAspArgMetThrSerVal----- 435  
 DB 1657 TGAGCCCGGTTCACCAAGACTCGGGTCAGTACAGACTGACGGCCATCTCAGTGACCA 1716  
 QY 436 -lleAlaThrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe 455  
 DB 1717 TTCAGCCGACCCCTCCAGCAATACACAGTATCTTCTTGCGCTGTGAAGTGCATGCT 1776  
 QY 455 ulysLysile----- 458  
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 QY 459 -----ArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal 476  
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 DB 1936 GGGCTTCTCTAGCTGCATATCCGATCCCTCCTCAGTGTGAGCCTTATGATCATG 1995  
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RESULT 15  
 US-09-653-274-5  
 ; Sequence 5, Application us/09653274  
 ; Patent No. 6635742  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, Bryan J  
 ; APPLICANT: Yeung, George Y  
 ; APPLICANT: Arterburn, Matthew C  
 ; APPLICANT: Mize, Nancy K  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenchua  
 ; APPLICANT: Drenth, Kadoje T  
 ; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like  
 ; FILE REFERENCE: HVS-23  
 ; CURRENT APPLICATION NUMBER: US/09/653,274  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: 09/491,404  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 3261  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-653-274-5

Alignment Scores:  
 Pred. No.: 1,45e-13 Length: 3261  
 Score: 228.00 Matches: 128  
 Percent Similarity: 37.30% Conservative: 101  
 Best Local Similarity: 20.85% Mismatches: 224  
 Query Match: 2,288 Indels: 162  
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QY 30 ProAlaProLeuSer-----GlnLysGlnArgSerPheValThrPheArgGly 45  
 DB 79 GATGAACCCCTTAATATCTGTCATATCACTTATCAAGCAATATCCGTTTATGAGCA 138  
 QY 46 GluProAlaGluGlyPheAsnHisLeuValValAsp-----GluArgThr 60  
 DB 139 CGGCTTCAGGCAATGAATGCGACAGCAGCTGACCTTCAGCTGATGTGAATTCGA 198  
 QY 61 GlyHisIleTyrLeuGlnValAlaValAsnArgIleTyrLysLeuSerSerAspLeuVal 80  
 DB 199 GACACCTTATATGCTGCGCAGGAGTCAAGTTTATACAGTA-----AACTTAATGA 252  
 QY 81 LeuValThrHisGluThrGlyProAsp-----GluAsp 91  
 DB 253 ATGCCCAAAACAGAGTATATACCAACAAAGAAATGACATGCGCATCAAGACAGCAT 312  
 QY 92 AsnProLysCys---TyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 110  
 DB 313 CGAAGAACTGTGCTATGAAAGCAAGATGAATGAAATGCAACTTATTC----- 366  
 QY 111 ThrAsnValAsnLysMetLeuLeuLeuAspTyrLysGluAsnArgLeuIleAlaCys 130  
 DB 367 -----AAAGTATTGTTCGAAGAAACGATGAGATGTTTGTGTTGT 408  
 QY 131 Gly---SerLeuTyrGlnGlyTyrLysLysLeuLeuValGluGlnAspLeuPheLysLeu 149  
 DB 409 GGTACCAATGATTCATTCATCCATGTGTAGTACTACAGGTTAGTACCTTAGAATATGAT 468  
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 DB 469 GGGAGAGAA-----ATTAGTGGCTTCGCAAGATGCCATTGAT 507  
 QY 164 -----AsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 181  
 DB 508 GCCAGCAACCAACATGTCCTCCCTTGTCT-----GATGG 543  
 QY 182 LysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSer 201  
 DB 544 AGCTGTATTCGCGCACAGTGGCTGAC-----TTCTTGCGCAC 582  
 QY 202 ArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGlu 221  
 DB 583 GATGCCGTATTATTAGCAAGCATGGGTGATGATGCTCCCTTCGACACATA-----AAA 636  
 QY 222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241  
 DB 637 TATGATTCCAATGATTAAGACCA----- 663  
 QY 242 IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro 261  
 DB 664 ---CACTTCTTCATGACCATAGAAATGAGAACTATGCTATTCTTCTTCGAGAA--- 717  
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 QY 293 TyrValGluValProIleGlyCysGluArgSerGly-----Val 305  
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 QY 306 GluTyrArgLeuLeuGlnAlaIleTyrLeuSerLysAlaGlyAlaValLeuGlyArgThr 325  
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QY      376 ArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSer 395
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QY      396 Ala-LeuLeuThrIleAsp-----AspAsnPheCysGlyLeuAspMetAsnAlaProLe 413
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QY      413 uGlyValSerAspMet-----ValArgGlyIleProValPheThrGluAsp-----Ar 429
Db      1194 GATGACCTCTGCCGTTCCACCCATTCGCGATGAGCCCTGTTCACAAAGACTCGGCTCAG 1253
QY      429 GAspArgMetThrSerVal-----IleAlaTyrValTyrLysAsnHisSerLe 445
Db      1254 GTACAGACTGACGGCCATCTCAGTGCACCATTCAGCCGACCTTACCAAGACTACACAGT 1313
QY      445 uAlaPheValGlyThrLysSerGlyLysLeuLysLysIle----- 458
Db      1314 CATCTTTGTTGGCTCGAAGCTGGCATGTGTACTTAAGTTCTGGCAAGACCAAGTCTTT 1373
QY      459 -----ArgValAspGlyProArgGlyAs 466
Db      1374 CTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAAGCTTACCAACCATGCAAGTGCAG 1433
QY      466 nAlaLeuGlnTyrGluThrValGlnValAlaAspProGlyProValLeuArgAspMetAl 486
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GenCore version 5.1.6  
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Run on: February 20, 2004, 12:46:42 ; Search time 938 Seconds  
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Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	6267.5	62.7	5895	12	US-10-087-684-31	Sequence 31, Appl
3	6267.5	62.7	5895	12	US-10-218-779-31	Sequence 31, Appl
4	2560	25.8	6252	9	US-09-964-824A-113	Sequence 113, App
5	2560	25.8	6252	10	US-09-930-213-254	Sequence 254, App
6	2029	20.3	3666	15	US-10-108-260A-802	Sequence 802, App
7	1372	13.7	2597	14	US-10-245-103-81	Sequence 91, Appl
8	1372	13.7	2597	14	US-10-245-103-81	Sequence 91, Appl
9	1372	13.7	2597	14	US-10-245-143-81	Sequence 91, Appl
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14	1372	13.7	2597	14	US-10-238-183-81	Sequence 91, Appl
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39	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl
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41	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl
42	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl
43	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl
44	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl
45	1372	13.7	2597	14	US-10-245-730-81	Sequence 91, Appl

## ALIGNMENTS

RESULT 1  
US-10-175-523-95  
Sequence 95, Application US/10175523  
Publication No. US20030096264A1  
GENERAL INFORMATION:  
APPLICANT: Brockman, Jeffrey  
APPLICANT: Evans, David  
APPLICANT: Hook, Derek  
APPLICANT: Klimczak, Leszek  
APPLICANT: Laeng, Pascal  
APPLICANT: Palfreyman, Michael  
APPLICANT: Rajan, Priithi  
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHATS)  
FILE REFERENCE: 3235/1J795-US3  
CURRENT APPLICATION NUMBER: US/10/175,523  
CURRENT FILING DATE: 2002-06-18  
PRIOR APPLICATION NUMBER: US 60/299,151  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: US 60/317,828  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: US 60/325,150  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/333,047  
PRIOR FILING DATE: 2001-11-14



PRIOR APPLICATION NUMBER: US 60/349,936  
 PRIOR FILING DATE: 2002-01-18  
 PRIOR APPLICATION NUMBER: US 60/361,834  
 PRIOR FILING DATE: 2002-03-04  
 NUMBER OF SEQ ID NOS: 197  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 95  
 LENGTH: 6730  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(6730)  
 OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other  
 US-10-175-523-95

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score:	6765.00	1268	239	357	14
Percent Similarity:	80.24%				
Best Local Similarity:	67.52%				
Query Match:	67.72%				
DB:	14	Gaps:	8		

US-09-964-956-13 (1-1896) x US-10-175-523-95 (1-6730)

25 LeuLeuThrArgGlnProAlaProLeuSerGlnLeuSerPheValThrPheArg 44  
 628 CTGCTAGCTCTGGGACACAGATAGCTCAG-----TACACACTTTCAC 675  
 45 GlyIuProAlaGlu--GlyPheAsnHisLeuValAlaSerGluValThrGlyHisIle 63  
 676 TCTGAGATCGTCACTGACCTTCAACCATTTGACTACACCGAAGAAAGGGGCTGTG 735  
 64 TyrLeuGlyAlaValAsnArgIleTyrIleuSerSerAspLeuValIleValThr 83  
 736 TATGGGGGGCTACCAATCGTCTCAAGTTGACTGGCAACCTCACCATCCAGGTGGCT 795  
 84 HisGluThrGlyProAspGluAspAsnProLysCysTyrProProAlaGlnIleThr 103  
 796 CACAGACAGGGGCCAGAGAGACACAGAGCTTGTACACCCCTCATTTGACAGCCC 855  
 104 CysAsnGluProLeuThrThrThrAspAsnValAsnLysMetLeuLeuLeuValLys 123  
 856 TGCAGTGAAGTCTTACCTACCTACCAACATGTCAACAACTGATGATGACTACTCT 915  
 124 GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu 143  
 916 GAGATCGCTGCTGGCTGGCGAAGCTCTACCAAGGCTGTTCAGAGCTCTGCGACTA 975  
 144 GluAsnLeuPheLysLeuGlyLysProLysHisLysLysGlnHisTyrLeuSerGlyVal 163  
 976 GATGACCTCTTCATCTCTGGTGGAGCCATCCCAAGAGAAACCTTCTGTCAGATGTC 1035  
 164 AsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLeu 183  
 1036 AATAAGACAGGACCATGTATGTGTGTGCTGCGCTCTGAGGGGAGAGATGGCAACCTT 1095  
 184 PheIleAlaThrAlaValAlaAspGlyLysProGluTyrPheProThrIleSerSerArgLys 203  
 1096 TTATCGGACCTGCTGTGATGGAGCAGAGGATTACTTCTCTACTCTGTCAGGCGGAG 1155  
 204 LeuThrLysAsnSerGlyAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal 223  
 1156 CTGCCCCGTAACCTGAGCTTTCAGCAATGCTGAGCTATGAGCTCCACAGATTTGTC 1215  
 224 AlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTyr 243  
 1216 TCTTCCCTCATCAAAATTCCTCTGACACCTTACCTGCTCTCACTTGAACATCTTC 1275  
 244 TyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMet 263  
 1276 TACATCTATGCTTTGGCAGTGGGGGTTTGTCTACTTCTCAGCTGTCAGCCAGAG-- 1332

264 ValSerProProGly-----SerThrThrLysGlnGlnValTyrThrSerLysLeu 280  
 1333 ---ACCCCTGACGGCATGCGCATCAATTCAGCTGAGACCTCTTATCTCAAGAAATT 1389  
 281 ValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCys 300  
 1390 GTGCTCTCTGGAAGATGAGACCCCAAGTTCATCTGTATGTGCTCCCTTTGGCTGC 1449  
 301 GluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerValAlaGlyVal 320  
 1450 ACACGTGCTGGGGTGAATATGCTTCTGACAGGACCTTCTGCAAGCCAGGGGAA 1509  
 321 ValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSer 340  
 1510 GCTTAGCTCAGAGGCTTCACATCAGCAGCAGCAAGATGCTGTGTGACCATCTTTCC 1569  
 341 LysGlyGlnLysArgLysMetLysSerLeuSerProGluSerAlaLeuCysAlaPheIleLeu 360  
 1570 AAGGGGCAAGACAGTACACACACCCCTGATGACTGTGCTCTGTGCTTCCCATC 1629  
 361 LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr 380  
 1630 CGGGCATCACTTGCAATCAAGAGCGGTGAGCTCTGCTACACAGGAGGGCAAC 1689  
 381 LeuAspLeuAlaTrpLeuLysValIleAspIleProCysSerSerAlaLeuLeuThrIle 400  
 1690 TTGAGCTCAACTGCTCTGCGAAGATGTGACGTGACACCAAGCCCTGTGCCAATC 1749  
 401 AspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArg 420  
 1750 GATGATTACTTCTGGCTGGCTGGACATCAACAGCTCTGGAGGCTCCACCTGTGAG 1809  
 421 GlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyr 440  
 1810 GGACTGACCTCGTATACACACAGCAGGAGCGCTGACCTGTGTGCTCTCATGTGTAC 1869  
 441 LysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysIleArgVal 460  
 1870 AATGGCTACAGTGTGTTTGTGGGACTAAGATGGCCAGTCAAGATTCAGACT 1929  
 461 AspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal--AspProGly 479  
 1930 GATGTCCTCCCAAGGCGGCTCCAGTATGATGATGCTCTGTGTTCAAGATGGAGC 1989  
 480 ProValIleuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499  
 1990 CCAATCTCCGGGACATGGCTCTTCCATCAATCACTATCACTATGCTATGCTAG 2049  
 500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519  
 2050 AGCAGGTGACACAGGCTCCCTGTGATCAATGTGAACAGTATCACTGTGGAGAGGT 2109  
 520 LeuGlySerGlyAspProHisCysGlyTyrProCysValLeuHisAsnThrCysThrArgLys 539  
 2110 CTAGCTCAGGGGATCTCTACTGTGTGTGTGTGCTTGCCTGCACAAATGTGCTCCGAAGA 2169  
 540 GluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysVal 559  
 2170 GACAAATGCCAAGGGCTGGGAGACAAATGATTTGCTGCGACAGATACAGCCAGTGCATG 2229  
 560 ArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuValIle 579  
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 580 GluThrTyrAsnValProGluLeuSerAlaGlyValAsnGlyThrPheGluAspLeuSer 599  
 2290 GTTGTGAAGATGATCCCAACTCTCTGAAGTATGCTGTGCTGTGCTGTGCTGTGCTGT 2349  
 600 GluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGlu 619  
 2350 GAGGTGAGAGGACAGATATCTGGAGTCAAGTCACTGATCTCACTGACCCAGAGAT 2409

QY 620 ValProArgIleIleThrGluAsnGlyAspHisIleValGlnLeuGlnLeuSer 639  
 Db 2410 GTCCCT---GTCATCCCTCTGGATCAAGATCGTGTGGCTTAGAGCTGCAGCTGAGATCC 2466  
 QY 640 LysGlnThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnGlySerValHis 659  
 Db 2467 AAAGAGACAGGAAGATCTTTGTGACAGCAGCAATTCAGTTCTATACCTCAGAGCCAC 2526  
 QY 660 AsnSerCysLeuSerCysValGluSerProTyrArgGlyHisIleTyrCysValTyrArgHis 679  
 Db 2527 CAATGTCCTGCTCTGTGTGTACAGAGCCCTCCGCTGCGCATTTGGTCAAGTACCTTAC 2586  
 QY 680 ValCysThrHisAspProLysThrCysSerPheGlnGlnValArgValLysLeuProGlu 699  
 Db 2587 CTCTGCACACATGACCCCACTACTGTTCTTCCAGAGAGGAGGATCAATGTTTCAGAG 2646  
 QY 700 AspCysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysPro 719  
 Db 2647 GACTGTCCCGACGCTGTGCCCCAGAGAGATTCTGATCCAGTTGGGGAAGTAAACCA 2706  
 QY 720 IleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyIleArgGlyTyrGluCys 739  
 Db 2707 ATCACTTAAAGCCCGCAAACTGCTCCAGCCCAAGTCTGGCCAGCGAGCTACAGAGTGT 2766  
 QY 740 IleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSer 759  
 Db 2767 GTGCTCAGCATTTCAAGGGGGTGTCCACCGGGGTCCCTCCCTCCCTTCAACAGTTCCAGT 2826  
 QY 760 ValGlnCysGlnAsnThrSerTyrSerTyrGlnGlyMetGlnIleAsnAsnLeuProVal 779  
 Db 2827 GTGAGTCCCAAAACGCTGTACAGATGTGATGGATGACATCAGCAACCTTAGCATG 2886  
 QY 780 GluLeuThrValIleTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal 799  
 Db 2887 GACTTGTGTAGTATGATGATGAGCACTCATTTATTCACAACTCCAGCACTGAAAGTA 2946  
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 QY 820 AspPheAlaCysGlyTyrCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro 839  
 Db 3007 AAGTTCAAGTGTGTGTGTGACGTGTGAGCGCAGATGTACCTCCACAGCACTGCCCC 3066  
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 Db 3067 AGCACTTCTAGCCCTGCTGCTGACGTGTGACGCCAGCAATGTCAAGTGTCCAAACCCCAA 3126  
 QY 860 IleThrGlnIleIleProValIleThrGlyProArgGlnGlyIleThrLysValThrIleArg 879  
 Db 3127 ATCAACAGATTTTACAGATACAGATCAGACCACTGAGAGAGGAGCTCGTGTACATCAT 3186  
 QY 880 GlyIleAsnLeuGlyLeuGlnPheArgAspIleAlaSerHisValLysValAlaGlyVal 899  
 Db 3187 GCGCGAAGCTGGGCTGTGACTTCTCTGAGATGTGTCAACATGTGCGAGTGGCTGGAGTG 3246  
 QY 900 GluCysSerProLeuValAspGlyTyrIleProAlaGlnGlnIleValCysGluMetGly 919  
 Db 3247 CCTTCAACCTTATCCAGGGGAAATACATCGCTGAGCAAGTGTGTGTGAGATGGGC 3306  
 QY 920 GluAlaLysProSerGlnHisAlaGlyPheValGlnIleCysValAlaValCysArgPro 939  
 Db 3307 CATGCCGTTATAGTACCAACATCTGGGCTGTGAGCTGTGATGGGAGATGCAAGCCA 3366  
 QY 940 GluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetGlnLeuThrLysSerAspLeu 959  
 Db 3367 GAGTTCAAGACCAAGTCCCAAGCAAGATACCTTTTGATCTCTGTGTGTGTCTGATC 3426  
 QY 960 LysProSerArgGlyProMetSerGlyIleThrGlnValIleThrGlyThrAsnLeu 979  
 Db 3427 AGCCGATCCCGGAGCAAGATCAGAGGTACAGATGTACCAATCAGCGCATTAACCTT 3486  
 QY 980 AsnAlaGlySerAsnValValValMetPheGlyLysGlnProCysLeuPheHisAlaArg 999

Db 3487 GGTGCTGGGAGAGGTGGCAGTGTACCTGGGCAATCAGACCTGTGAATTCATGTGGAGG 3546  
 QY 1000 SerProSerTyrIleValCys---AsnThrThrSerSerAspGluValLeuGluMetLys 1018  
 Db 3547 TCATGATGATGATTTGATGTGTGTTTACCCCCCATATCATGATGATGAGCAGACCTCCT 3606  
 QY 1019 ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu 1038  
 Db 3607 GTCTCGAGAGTGTGACAGAGCCCGGGGTAGTACAGTCTGACATTCAGATGTATAGAT 3666  
 QY 1039 AspProThrIleValArgIleGluProGluTyrPheIleValSerGlyAsnThrProIle 1058  
 Db 3667 GACCCACGGGTCCAAAGTATGAGCAGAGTGGAGATACCTAGTGGGCACACACCTCA 3726  
 QY 1059 AlaValTyrGlyThrHisIleuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly 1078  
 Db 3727 ACCATCAAGGCTTCAACTGTGATGTCTATTCAGAGCCAGGCTCCAGTCAATTTAAT 3786  
 QY 1079 GlyLysGlnHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAla 1098  
 Db 3787 GCGAAAGATCTGTCAATGTATGACAGTGTAAACACACCACTCACTGTGTGCA 3846  
 QY 1099 ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPhe 1118  
 Db 3847 CCTCTCTGACCAAGTACTCCGCCAGGTCTGGACACTGTGGAAAGCGCCAGATGAGTTT 3906  
 QY 1119 GlyPheIleLeuAsnValAlaGlnSerLeuLeuIleAsnLysThrAsnPheThrTyr 1138  
 Db 3907 GGATTTCTCTTAAACATGTTCATCTTACTCACTTAAAGCAACCAAGTTCACTAC 3966  
 QY 1139 TyrProAsnProValPheGlnAlaPheGlyProSerGlyIleLeuGlnLysProGly 1158  
 Db 3967 TACCCCAACCAAGTGTGAATGTCTGACCCCACTGGAATGTGGATGAGAGCCAGCC 4026  
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 Db 4027 TCACCATCATCTGAAGGGCAAAATCTGTCTCTGCTCGCTGTGAGAGG---GCCAAA 4083  
 QY 1179 LeuAsnTyrThrValLeuValGlyLysProCysThrValThrValSerAspValGln 1198  
 Db 4084 CTCAACTACAGATGATGATGTGAGAGACACTTGTACAGTACATGTGTCTAGACACAG 4143  
 QY 1199 LeuLeuCysGluSerProAsnLeuIleGlyArgHisLysValMetAlaArgValGlyGly 1218  
 Db 4144 CTGCTTTGTGAACCTCCCACTCAAGGCGAGCAAGAGTATGATGATGACGTGGCGGG 4203  
 QY 1219 MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla 1238  
 Db 4204 ATGGTGTCTCACTGGGCTCCGTGAGCGTCATCTCCGACAGGCTGTGACCTGTCCAGCG 4263  
 QY 1239 IleValSerIleAlaValAlaGlyLysLeuLeuIleIlePheIleValAlaValLeuIle 1258  
 Db 4264 ATCATACAGATGAGCACTGTGAGAGCTGTGAAAGCTCTTCTTTATCATGTCTATCAT 4323  
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 Db 4324 GCTTAAACCGCAGCTGAGGAAATGACCTCAACCTCAACCGGCTCCAAATGCAAAAG 4383  
 QY 1279 AspAsnLeuGlnSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThr 1298  
 Db 4384 GACACCTGAGTCCAGGGTGGCATGTGAGTGCAGAGAGAGCTTTTCCGAGCTTCAGACA 4443  
 QY 1299 AspIleHisGlnLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArg 1318  
 Db 4444 GACATCAATGATGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 4503  
 QY 1319 ThrTyrThrMetArgValLeuPheProGlyIleGluAsnHisProValLeuArgAspLeu 1338  
 Db 4504 ACCTATGCCATGAGATCTGTCCAGGCAATGAGACCAACCTGTCTGTGGGAACTG 4563  
 QY 1339 GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeu 1358

Db 4564 GAGGTACAGGGAATGACAGACAGACGTGAGAGAAAGCCCTGAACTCTTGGCCAGCTT 4623  
Qy 1359 ILeuAsnLysValPheLeuLeuSerPheLeuThrLeuGlnLeuSerGlnArgSerPhe 1378  
Db 4624 ATCAACAACAAGAGTCTTCTGCTGACCTTCACTCCGATCCGATGAACTACAGCCCACTTC 4683  
Qy 1379 SerMetArgAspArgGlyAsnValAlaSerLeuLeuMetThrValLeuGlnSerLysLeu 1398  
Db 4684 TCCATGCGAGACCGTGGGAAAGTGGCTCTCTCATCTGACAGAGCTCTCAAGGCTCCCTTA 4743  
Qy 1399 GlnLysValAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuLeuAspLysAsnLeuGln 1418  
Db 4744 GAATATGCACTGATGTCCTTCAACAGAGCTGCTCTCACTTCACTTGAACAAAGCTGGAG 4803  
Qy 1419 SerLysAsnHisProLysLeuLeuLeuArgThrGlnSerValAlaGlnLysMetLeu 1438  
Db 4804 AACAAAGAACCCCAAGCTCTCTCCGACAGACTGATCTGTGGCCGAGAAAGATGCTG 4863  
Qy 1439 ThrSerPheMetThrPheLeuLeuLysLysPheLeuLysGlnCysAlaGlnLysPheLeu 1458  
Db 4864 ACTAAGCTGTTGCTTCTTCTTCAACAAGTCTCTGAAAGAGTGTGCTGGGAAACCACTC 4923  
Qy 1459 PheSerLeuPheCysAlaAlaLeuGlnMetGlnLysGlnLysProLysAspAlaLeuThr 1478  
Db 4924 TTCATGCTATACTGTGCATCAAGACAGACAGATGAGAAAGCCCATTTGACGCTATTACT 4983  
Qy 1479 GlnLysValAlaArgLysSerLeuSerGlnAspLysLeuLeuArgGlnGlnLeuAspLysLys 1498  
Db 4984 GGTAGAGCCCATCTCTCCGTAAGTAAGAACAGCTCCGCGACAGATGAGTAAAG 5043  
Qy 1499 ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGlnValProValLys 1518  
Db 5044 ACTCGATCCTGAAGCTGTGTCAACCTGACATGACATGAGAACGCCAGATGCCAGTGAAG 5103  
Qy 1519 IleLeuAsnCysAspThrIleThrGlnValLysGlnLysLysLeuAspAlaLeuPheLys 1538  
Db 5104 GTACTAAACTGTGACACCATCACTCAAGTCAAGAGAGAGATCCCTGATGCGATATTAAG 5163  
Qy 1539 AsnValProCysSerHisArgProLysAlaAlaAspMetAspLeuGlnLysPheArgGlnLys 1558  
Db 5164 AATGTCCTCTACTCCACGCGGCCAAGGCTGTGACATGATCTCGAGCTGGCCGCAAGGC 5223  
Qy 1559 SerGlnAlaArgMetIleLeuGlnAspLysLysLysLeuThrLysLysLysLysAsnAspTrp 1578  
Db 5224 CGGATTCGACAGAGTGTGTGTCAGAGACGACATTCACCAAAATAGAGGGGTGATGCG 5283  
Qy 1579 LysAspLeuAsnThrLeuAlaHisThrGlnValProAspGlnSerValAlaAlaLeuVal 1598  
Db 5284 AAGCGCTTAACACTGATGATCAATTCAGAGTGCACAGACAGATCCGTGGTGGCTGTGTT 5343  
Qy 1599 SerLysGlnValThrAlaLysAsnAlaValAsnAsnSerThrValSerArgThrSerAla 1618  
Db 5344 CTTAAGCAGAGCTCTCTCTCAACAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5403  
Qy 1619 SerLysLysLysAsnMetLysArgThrGlnLysProAspSerLeuArgSerArgThr 1638  
Db 5404 AGCGATATGACTCTCTCTCAAGGTACAGAGACCCAGACAGACCTCCGCTCCGCGGTC 5463  
Qy 1639 ProMetIleThrProAspLeuGlnLysGlnLysMetTrpHisLeuValLysAsnHis 1658  
Db 5464 CCGATGATCAACCCAGACTGTGAGAGCGGTGTCAAGGTTTGGCATCTGGTGAAGATCAT 5523  
Qy 1659 GlnHisGlnLysAspGlnLysGlnLysAspArgLysSerLysMetValSerGlnLysLeu 1678  
Db 5524 GACCATGTGTGACCAAGAGAGGTGACCGGAGCGCAAAATGTGTCTGAGATCTACTTG 5583  
Qy 1679 ThrArgLeuLeuAlaThrLysGlnLysLeuGlnLysPheValAspAspLeuPheGlnThr 1698  
Db 5584 ACCGCGCTTTAGCCACCAAGGAGCCCTGCAAGATTTGTGACAGCTTGTGGAAGCC 5643  
Qy 1699 IlePheSerThrAlaHisArgGlnSerLysLeuProLeuAlaLysLysLysMetPheAsp 1718  
Db 5644 TTGTCAGACACTGTACCCGGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5703

Qy 1719 PheLeuAspGlnGlnAlaAspLysHisGlnLysLysAspProHisValAlaGlnHisThrTrp 1738  
Db 5704 TTTCTGATGACAGAGGACAGACACAGATCCACACACAGATGTGGCGACACCTGG 5763  
Qy 1739 LysSerAsnCysLeuProLeuArgPheThrValAsnMetIleLysAsnProGlnPheVal 1758  
Db 5764 AAGACCACTGCTTCACTTCTGTTCTGGGTGAATGTCATCAAGAACCTCAATTTGTA 5823  
Qy 1759 PheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPhe 1778  
Db 5824 TTGACATCCCAAGAGGACGATCAAGATCTCTGCTCTGTGTGTAAGCCCAAGCTTT 5883  
Qy 1779 MetAspSerCysSerThrSerGlnHisArgGlnLysAspSerProSerAsnLysLeu 1798  
Db 5884 ATGACCTCTGTTCACATCAAGAGACCGACTGAGCAAGGACTCACTTCCACAGACTG 5943  
Qy 1799 LeuValAlaLysAspIleProSerThrLysAsnTrpValGlnArgLysSerAspIle 1818  
Db 5944 CTTATGCAAGATATCCCAAGTATTAAGATCGGTAGAAAGTACTATGACAGATAT 6003  
Qy 1819 GlnLysMetProAlaIleSerAspGlnAspMetAsnAlaThrLeuAlaGlnLysSerArg 1838  
Db 6004 GCCAAGCTCCCAAGCCATTAAGTACCAAGATATGATGCTTCTGCGAGACAGTCCGC 6063  
Qy 1839 MetHisMetAsnGlnPheAsnThrMetSerAlaLeuSerGlnLysPheSerThrValGln 1858  
Db 6064 CTGATGCTACAGAGTTCAATATGCTGAGCCGCCCTCAACGAGATCTACTATATGTCAGC 6123  
Qy 1859 LysLysSerGlnLysLysLeuGlnLysProLeuAspHisAspAspGlnCysGlnLysGlnLys 1878  
Db 6124 AAGTCACTGTAGAGACTCATCTGCGGCACTTAAGCAGATGTAACAGGCCGCAAGCAAG 6183  
Qy 1879 LeuAlaThrLysLeuGlnLysValIleThrLeuMetSerLeuAspSerAsnLys 1896  
Db 6184 CTGGCTTACAGGTGAGACATCTCAACCCGATGTCATAGAGAGCTGAAG 6237

RESULT 2  
US-10-087-684-31  
Sequence 31, Application US/10087684  
Publication No. US20040029116A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: MacDougall, John R.  
APPLICANT: Willet, Isabelle  
APPLICANT: Elberman, Karen  
APPLICANT: Stone, David J.  
APPLICANT: Grosse, William M.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Li, Li  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Mishra, Vishnu  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Rastelli, Luca  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Zernusen, Bryan D.  
APPLICANT: Malyanekar, Uriel M.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Miller, Charles E.  
APPLICANT: Gangoli, Esma A.  
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-214 CIP  
CURRENT APPLICATION NUMBER: US/10/087,684  
CURRENT FILING DATE: 2003-03-10  
PRIOR APPLICATION NUMBER: 60/253,834  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: 60/250,926



QY	583	AsnVal.ProdiuLeuSerAlaGlyValAlaSerCysThrPheGlnuAspLeuSerGluMetAsp	602
Db	1841	AAAGTGGCTTAAGCTCTCAAGCTGGCGGTCAACTGCTCTCCAGACCTTCAACGGATCTGAG	1900
QY	603	GlyLeuValValGlyAanglnIleGlnCysTyrSerProAlaAlaGlyValProArg	622
Db	1901	AGCTCTGTGAGAGATGACCGGATTCACCTGGCCGCTCACCTCCGCGCGGGAGGTGGCGCC	1960
QY	623	IleIle-----ThrGluAenGlyAspHisHisValValGlnuGlnuLeuLysSerTyr	640
Db	1961	ATCAGCGGGGCGCCAGGGTGAGGGAGACACAGCGGGGTGTGAATCTTCAACTTAAGTCCAG	2020
QY	641	GluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHis--	659
Db	2021	GAGCAGGGAGAAAGATTGGCTGCTGTGGACTCTGCTTTCATCAACTGCACCGTCCACAG	2080
QY	660	AsnSerCysLeuSerCysValGluSerProTyrArgCysHisIleTPCylsTyrArgHis	679
Db	2081	TCGAGCTGCTCTGCTGTGTCAAGGCTCTTCCCTCCAGCTGTGTCAATACCGGCAC	2140
QY	680	ValCysThrHisAspProLysThrCysSerPheGlnuGlnuValLysLeuProGlu	699
Db	2141	GTGTGCACACCAACAGTGGCTGACTGGCCCTTCTCGAGGGCCGTGTCAACGGTGTGAG	2200
QY	700	AspCysProGlnuLeuLeuArgValAspIleLeuValProValGluValIleLysPro	719
Db	2201	GACTGCCCAAGATCTGCCTCCACGACAGATCTACGTGCCAGTGGGAGTGTAAACCC	2260
QY	720	IleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyAlaGlyTyrGlnCys	739
Db	2261	ATCACCCTGGCGGCACGGAACCTGCACAGCACAGTCAAGCCAGCGTGAATAGATGC	2320
QY	740	IleLeuAsnIleGlnGlySerGlnuGlnuArgValProAlaLeuArgPheAsnSerSer	759
Db	2321	CTCTTCCACATCCCGGAGCGCCGCGCGCTGTCAACGCGCTTCAACAGCTCCAGC	2380
QY	760	ValGlnCysGlnuAsnThrSerTyrSerTyrGlnuLysMetGluIleAsnAsnLeuProVal	779
Db	2381	CTGCAGTCCCAAGATTCCTGTACTCCCTACAGGAGGAGAACGATGTCAGGACTTCCAGTG	2440
QY	780	GluLeuThrValIleTyrAsnGlyHisIlePheAsnIleAspAsnProAlaGlnAsnLysVal	799
Db	2441	AACCTGTAGTGTGTGTGAACGGCAACTTGTCAATTGACAAACCAACATCCAGCGC	2500
QY	800	HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPro	819
Db	2501	CACCTCTCAAAAGTGGCGGCGCTGTGGCAGAGCTGGCGCTGTCTAAAGCGAAGCCG	2560
QY	820	AspPheAlaCysGlyTyrCysGlnuLysProGlyGlnuSerThrLeuArgGlnHisCysPro	839
Db	2561	CGCTTCAGATGGAGATGGGTGGCGGACGAGCGCGCTGCTCCCTGCACACACTGCGCT	2620
QY	840	AlaGln---GluSerGlnThrLeuGlnuLeuSerGlyAlaLysSerLysCysThrAsnPro	858
Db	2621	GCGGACACACCTGCATCGGTGATGAGACGCGCGCTCACGCGACAGATCGGTGACCAAGCC	2680
QY	859	ArgIleThrGlnuIleIleProValThrGlyProArgGlnuGlyGlyThrLysValThrIle	878
Db	2681	AAGATCTCAACAGTGTCCCGCCGAGACGGGCGCGGAGCGAGGGCGGACCGGCTCACTATC	2740
QY	879	ArgGlyGluAsnLeuGlyLeuGlnuLysPheArgAspIleAlaSerHisValLysValAlaGly	898
Db	2741	ACAGCGAGAACTGGGCGCTGGATTCGAAGCGTGTGGGTGGCGGTGGCGGCAAG	2800
QY	899	ValGlnCysSerProLeuValAspGlyTyrIleProAlaGlnuGlnuIleValCysGluMet	918
Db	2801	GTGCTGTGACGCGCTGTGAGAGCAGATACATCACTGGCGAGCAATGCTGTGTGAGATC	2860
QY	919	GlyGlnuAlaLysProSerGln---HisAlaGlyPheValGlnuIleCysValAlaValLys	937
Db	2861	GGGAGCGCCAGCTCCGTGCTGCCATGACGCGCTGGTGGAGGTGTGTGTGGGAGATCTC	2920
QY	938	ArgProGluPheMetAlaArgSerSerGlnuLeuTyrTyrPheMetThrLeuThrLeuSer	957

Dc	2921	TCACCAACAGTACCGCGCCCTGTCAACCAAGCGCTTCACTTCCTGAGACCAACCTTCTTAC	2960
Qy	958	AspLeuLysProSerArgAGLYProMetSerGlyGlyThr:GlnValThrIleThrGlyThr	977
Db	2981	CGTGTAGACCCCTCCGCTGGGCTCTCTGACGGGGACCTGGATTGGCATCGAGGAGAC	3040
Qy	978	AsnLeuAsnAlaGlySerAsnValValValMetPheGlyLysGlnProCysLeuPhe---	996
Dc	3041	CACCTGAACGACGACATGATGTGGCTGTGCTGCTGCTGCGGCGCCCTGTCTCTTCTCC	3100
Qy	997	---HisArgArgSerProSerThrIleValCysAsnThrThrSerSerArgGluValLeu	1015
Dc	3101	TGTCTCCAGAGAACTCCCGTGAATCCGGTGTGCTGACACCCCGGGGCGAGGCGCTGAC	3160
Qy	1016	GluMetLysValSerValGlnValAspArgAlaLysIle---HisGlnAspLeuValPhe	1034
Dc	3161	AGCCCTCCCATCAATCAATCAATCAATCAACCGCGCCGAGTCAACCAACCTGAGTAAAGTAC	3220
Qy	1035	GlnIleValGluAspProThrIleValArgIleGluProGluTyrPserIleValSerGly	1050
Dc	3221	AACACACAGAGAACCCACCATCTCTGAGATCGAACCCGAGTGAAGCATCAACGCGGT	3280
Qy	1055	AsnThrProIleAlaValTyrGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArg	1074
Dc	3281	GAGACCCCTCCGACGGGTCAACAGGACCAACCTGGCCACTGTCGGTGAACCCCGAATCCGG	3340
Qy	1075	AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValIleAsnAlaThrGluMet	1094
Dc	3341	GCCAAAGTATGAGAGCATGTAGAGGAGAGAAC---TGCCTGGTGAATAGACACCCACATG	3397
Qy	1095	ThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArg	1114
Dc	3398	GTAATGCCCGCCCGCTGTGGGCCCAACCTGTGCGACGCCACCAACAGACTGGGGAGCGG	3455
Qy	1115	ProGluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThr	1133
Dc	3458	CCGATGATGCTGGGCTTGCTGATGAGCAACGGGGCTCCGCTGTGCTCAACTCCACAC	3511
Qy	1135	AsnPheThrIleTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGlu	1155
Dc	3518	TCCTTCCCTCACTACCTGACCCCGTACTGAGCCACTGACGCCACCTGAGGCTGCTGGAG	3577
Qy	1155	LeuLysProGlyLysProIleIleLeuLysGlyLysAsnLeuIleProProValAlaGly	1177
Dc	3578	CTGAAGCCCAAGCTCCCACTACTCTCAAGGGCCGGAACCTTGTCCACACT---GCACCC	3633
Qy	1175	GlyAsnValLysLeuAsnThrThrValLeuValGlyGlyLysProCysThrValThrVal	1199
Dc	3635	GCCAACTCCCACTCACTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3699
Qy	1195	SerAspValGlnLeuLeuCysGlnSerProAsnLeuIleGlyArgHisLysValMetAla	1211
Dc	3695	TGGAGACGCAACTGCTGTGGAGGCGGCCCAACTCACTGGGCGACACACAGGTCAAGGTG	3755
Qy	1215	ArgValIleGlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeu	1233
Dc	3755	CGTGAGGGGTTCGAGTTCTGCGACAGGACACTGCAAGGTACTCGACAGCGCTGCTG	3811
Qy	1235	SerLeuProAlaIleValSerIleAlaValAlaGlyLysLeuLeuIleIlePheIleVal	1255
Dc	3815	ACGTGCGCTGCATGTGGGCACTTGGCGAGGCGGGGCTTCCTCTGCTGTGTCATCGTG	3877
Qy	1255	AlaValLeuIleAlaTyrLysArgLysSerArgGlnSerAspLeuThrLeuLysArgLeu	1277
Dc	3875	GCTGTGCTCATGCGCTTCAAGCGCAAGTCAAGAGTGTGACCGGACATTCAGAGCGGCTG	3933
Qy	1275	GlnMetGlnMetAspAsnLeuGlnSerArgValAlaLeuGluCysLysGluAlaPheAla	1299
Dc	3935	CAGCTCCAGATGAGACAACTGAGAGTCCCGCTGGGCTTCGAAATGCAAGGAACCTTTGGA	3999
Qy	1295	GluLeuGlnThrAspIleHisGlyLeuThrSerAspLeuAspGlyValaGlyIleProPhe	1311

Db 3995 GAGCTGACAGACGATCCAGAGCTGACCAATGACCTGACGCTGCCGATCCCTTC 4054  
 QY 1335 LeuAspTyrArgThrTyrThrMetArgValLeuPheProGlyIleGluAspHisProVal 1334  
 Db 4055 CTGTAATCCGACATATGCCATGCGGGTCTCTTCTGGGATCGAGACACCCCTGTG 4114  
 QY 1335 LeuAspLeuGluValProGlyTyrArgGlnValGluValGlyLeuLeu 1354  
 Db 4115 CTCAAGAGATGAGGTA-----CAGGCCAATGTGAGAACTCCCTACACTG 4162  
 QY 1355 PheAlaGlnIleuIleAsnAsnValPheLeuLeuSerPheIleArgThrLeuGlnSer 1374  
 Db 4163 TTCGGGAGCTCTGACCAAGAGCACTTCTGCTGACCTTCATCCGACCTGAGGCA 4222  
 QY 1375 GlnArgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeu 1394  
 Db 4223 CAGCGCAGCTTCTCCATGCGGACCGCGGAAATGCGCTCGCATGACGCGCCCTG 4282  
 QY 1395 GlnSerTyrLeuGlnTyrAlaThrAspValLeuValGlnLeuAlaAspLeuIleAsp 1414  
 Db 4283 CAGGGGAGATGAAATACCCACAGCGCTGCTCAAGAGCTGCTTCGACCTCATGAG 4342  
 QY 1415 LysAsnLeuGlnSerTyrAsnHisProTyrLeuLeuLeuArgArg---ThrGlnSerVal 1433  
 Db 4343 AAGAACTGAGAGAGCAAGAACACCCCAAGCTGACTGCGCGGCAACTGACGCGTG 4402  
 QY 1434 AlaGlnLysMetLeuThrAsnTyrPheThrPheLeuLeuTyrTyrPheLeuLysGlnLys 1453  
 Db 4403 GCAGAGAAATGATCTAATCTAGCTTCACTTCTCTGTATTAATGTTCTTCAAGAGATGC 4462  
 QY 1454 AlaGlnGluProLeuPheSerLeuPheCysAlaIleTyrGlnGlnMetGlnLysGlyPro 1473  
 Db 4463 GCTGGGAGCCGCTGTTCACTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4522  
 QY 1474 IleAspAlaIleThrGlnValAlaArgTyrSerLeuSerGlnAspLysLeuIleArgGln 1493  
 Db 4523 ATGAGCGCATCAAGGAGGAGGACGCTCTCTCTGAGTGAAGAGACAACTCTCGGAG 4582  
 QY 1494 GlnIleAspTyrThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerPro 1513  
 Db 4583 CAATATGACTACAAAGACACTGACCCCTGAACCTGTGTGAACCTGAGATAGATGACACT 4642  
 QY 1514 GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlnLysIleLeu 1533  
 Db 4643 GAGGTGCGGTGAAGGGGCTGAGCTGTGACACGCTACCCAGGCCAAGAGAGCTGCTG 4702  
 QY 1534 AspAlaIlePheLysAsnValProCysSerHisArgProLysAlaAlaAspMetAspLeu 1553  
 Db 4703 GAGCGTGCCTACAAAGGCGCTGCTTCTCCAGCGGCCCAAGGCCGAGCATGACCTG 4762  
 QY 1554 GluThrArgGlnLysSerGlyAlaArgMetIleLeuGlnAspGlnAspIleThrThrLys 1573  
 Db 4763 GAGTGGGCGCAAGGCGCGCATGCGCGCATCATCTCGACAGACGAGACCTCACCAAG 4822  
 QY 1574 IleGluAsnAspTyrTyrValArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySer 1593  
 Db 4823 ATTGACAAACATTTGAAGAGCTGGAACACTGCTCACTACCAAGGAGACAGGAGCTC 4882  
 QY 1594 ValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnSerThrVal 1613  
 Db 4883 TCGGTGCACTGTGCGCCAAAGCAAGCTCGCGCTACAAACTCCCAACTCTTCACTTC 4942  
 QY 1614 SerArgThrSerAlaSerLysTyrGlnAsnMetIleArgTyrThrLysSerProAspSer 1633  
 Db 4943 ACCAAG---TCCCTCACAGATACAGAGACATGCTGCGACGCGCCAGCACTCCGACAG 4999  
 QY 1634 LeuArgSerArgThrProMetIleThrProAspLeuGlnSerGlyValLysMetThrHis 1653  
 Db 5000 CTGGGCTGCGCGACCCCATATATACCGCCGACCTGAGAGCGGCAACCAAGCTGTGGCAC 5059  
 QY 1654 LeuValLysAsnHisGlnLysGlyAspGlnLysGlnLysAspArgLysLysMetVal 1673  
 Db 5060 CTGGTGAAGAACCAAGCACTGAGCCAGCGTGAAGGCTGACCGCGGCAAGATGCTC 5119

QY 1674 SerGlnIleTyrLeuThrArgLeuLeuAlaThrLys---GlyThrLeuGlnLysPheVal 1692  
 Db 5120 TCGAGATCTACTTGAACAGGCTACTGCGCACCAAGGAGCACTGACAGAGATTGTG 5179  
 QY 1693 AspAspLeuPheGlnThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAla 1712  
 Db 5180 GAGCACTGTTTGAGACCATCTTTCAGACGAGCAACCGGGGCTGAGCCCTGCGCTGGCC 5239  
 QY 1713 IleLysTyrMetPheAspPheLeuAspGlnGlnAlaAspLysHisGlyIleHisAspPro 1732  
 Db 5240 ATCAAGTAACATGTTTCACTTCTCGATGACAGCGCGCAAGCAACCAAGATCAACGATGCT 5299  
 QY 1733 HisValArgHisThrTyrLysSerAsnCys---LeuProLeuArgPheThrValAsnMet 1751  
 Db 5300 GAGTGGCGCCACACCTCGAAGAGCAACTGACAGCTGCCCTGCGCTTCGGGTGAACGTG 5359  
 QY 1752 IleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAspAlaCysLeu 1771  
 Db 5360 ATCAAGAACCCACAGTTTGTTGTCGACATTCACAAAGACATCAACGAGCGCTGCTTG 5419  
 QY 1772 SerValValAlaGlnThrPheMetAspSerCysSerThrSerGlnHisArgLeuGlyLys 1791  
 Db 5420 TCGGTGTGCGCCAGACCTTCACTGACTCTGCTTCACTGACGACCAAGCTGGGCAAG 5479  
 QY 1792 AspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnThrVal 1811  
 Db 5480 GACTCACTCCCAACAAAGCTGCTCTAGCCCAAGACATCCCACTACAAAGACTGGGTG 5539  
 QY 1812 Gln---ArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsn 1830  
 Db 5540 GAGAGAGGTACATGAGACATGACATGCGCAAGATCCAGCCATTCAGCCAGACATGAGT 5599  
 QY 1831 AlaTyrLeuAlaGlnGlnSerArgMetHisMetAsnGlnPheAsnThrMetSerAlaLeu 1850  
 Db 5600 GCGATCTGCTGAGCAGCTCCCGCTGCACTGAGCAAGTCAACAGCATGAGCGCTTG 5659  
 QY 1851 SerGlnIlePheSerTyrValGlyLysTyrSerGlnLys-----IleLeuGlyProLeu 1868  
 Db 5660 CACGAGATCTACTCTTCATCACTACCAAGTACAGATAGGTGACAGATCTTGGACGCTG 5719  
 QY 1869 AspHisAspArgGlnCysGlyLysGlnLysLeuAlaTyrLysLeuGlnGlnValIleThr 1888  
 Db 5720 GAGAGCATGAGCAGGCGCGCGCGGCGGCTGCGAGCAAGCTGAGCGAGTGTGAGAC 5779  
 QY 1889 LeuMetSerLeuAspSer 1894  
 Db 5780 ACGATGCGCTGAGACAGC 5797

# RESULT 3

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 ; Publication No. US20040029222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: MacDougall, John  
 ; APPLICANT: Miller, Isabelle  
 ; APPLICANT: Ellemann, Karen  
 ; APPLICANT: Stone, David  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Grosche, William  
 ; APPLICANT: Alsbrook II, John  
 ; APPLICANT: Lepley, Denise  
 ; APPLICANT: Rieger, Daniel  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Casman, Stacie  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Patnajan, Meera  
 ; APPLICANT: Shenoy, Suresh





Db 1661 GACCCCACTGGCTGGTGTGTGTCTGTCAACAGCAATGTGTCTGGCGGGGAGCGCTGTGAG 172

Qy 544 ArgSerlySGluProArgArgPheAlaSerGluMetlySGlnCySValArgLeuThrVal 563

Db 1721 CGACCAAGCGAGCCCAAGCCGCTTGGCTGTCCGAGACCTGCGAGTGTGTGCACCTACACTGTG 1780

Qy 564 HisProAnaAniLeSerValSerGlnTyrAsnVal---LeuLeuValLeuGluThrTyr 582

Db 1781 CAGCCCCGCAATGTGTCTGTCAACCATGTCCAGGTCCAGATCACTGTGTCTCAAGCCCTGG 1840

Qy 583 AsnValProGluLeuSerAlaGlyValAlaAsnCysThrPheGluAspLeuSerGluMetAsp 602

Db 1841 AACGGCTCGACCTCTCAGCTGGCGTCACACTGCTCTCTTCGAGGACTTCACAGCAATCTGAG 1900

Qy 603 GlyLeuValValGlyAlaAsnGlnIleGlnCysTyrSerProAlaAlaGlyGluValProArg 622

Db 1901 AGCGTCGAGGAGATGGCCCGGATTCACCTGGCAGTCACTCCCTCCGCCCCGGAAGTGGCCCC 1960

Qy 623 IleIle-----ThrGluAsnGlyAspHisHisValValGlnLeuGlnLeuLysSerLys 640

Db 1961 ATCAGCGGGGGGCGACAGGTGAGGGAGAACAGCGGGGGTGGTGAACCTCACTTAAGTCCAAAG 2020

Qy 641 GluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHis--- 659

Db 2021 GAGACAGGAGAGAAAGTGGTGGCTGTGTGACATCTGCTTTCACATCGACGAGGTCCACAG 2080

Qy 660 AsnSerCySLeuSerCySValGluSerProTyrArgCysHisTyrCySLeuTyrArgHis 679

Db 2081 TCGAAGTGGCTGTCTGTGTGTCAAGGCTCTTCTCCCTCCACAGTGTCAAAATCCGCCAC 2140

Qy 680 ValCySThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGlu 699

Db 2141 GTGTGCACACACAAAGTGGCTGACGCGCTTCCGTGAGGGGCGGTGTCAACGTGTCTAGG 2200

Qy 700 AspCysProGlnLeuLeuArgValAlaAspHisIleLeuValProValGluValIleLeuAsp 719

Db 2201 GACTGCCCAACATCTGCTGCTCTCCACGCGAATCTACGTGCCAGTGGAGTGTATAAACCC 2260

Qy 720 IleThrLeuValAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCys 739

Db 2261 ATCAGCTGGCGCGCACAGGAACCTGCCACAGCCACAGTACAGGCCACGTGAGATATAGTGC 2320

Qy 740 IleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerSer 759

Db 2321 CTTCTTCAACATCCCGGAGCGCGCGCGCGGTGTACCGCGCTTGCGTTCAACAGCTCCAGC 2380

Qy 760 ValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVal 779

Db 2381 CTGCAGTGGCAAAATTCCTCTGTAATCTTACGAGGGAGACAGATGACAGCACTGCCAATG 2440

Qy 780 GluLeuThrValValIleTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal 799

Db 2441 AACCTGTCAAGTGTGTGAGAACGCGCAATTTGTCAATTGACACACCAAGAACATCCAGAGCG 2500

Qy 800 HisLeuTyrLysCySValAlaMetArgGlnSerCySValLeuCySLeuLysValAlaAsp 819

Db 2501 CACCTCTTACAAAGTGGCCCGCGCTCGCGCGAGAGTGGCGCTGTGCTCTCAAGGCCACAGCC 2560

Qy 820 AspPheAlaCySValTyrCySglnGlyProGlyGlnCysThrLeuArgGlnHisCySPro 839

Db 2561 CGCTTCAAGTGTGGAGATGTGTGTGGCGCGAGCGCCGCTGCTCTCCAGCACACACTGCGCT 2620

Qy 840 AlaGln---GluSerGlnTyrLeuGluLeuSerGlyAlaLysSerLysCysThrAsnPro 858

Db 2621 GCCGACACACCTGCATCGTGAATGCAACGCGCTCACGGGACAGCAAGTGGCTGCACCAACCC 2680

Qy 859 ArgIleThrGluIleIleProValThrGlyProArgGlnGlyIleThrLysValThrIle 878

Db 2681 AAGATCTCAAGTGTCTCCCGCGAGACGGGCGCGAGCAGAGGCGGACCGGCGCTCACTATC 2740

Qy 879 ArgGlyGluAsnLeuGlyLeuGluPheArgPheIleAlaSerHisValLysValAlaGly 898

Db 2741 ACAGGGCAAACTGGGCTGTGCAATTTCGAAGACGCGTCTGGCGCGTGGCGGAG 2800

QY	899	ValGlnGlySerProLeuValAspGlyTyrIleProAlaGlnGlnIleValCysGlnMet	918
Db	2801	GTCGTGTCAGCCCTGTGGAGAGCGAGTACATAGTCGGAGACAGATCGCTGTGGATC	2860
QY	919	GlyGlnAlaIalysProSerGln---HisAlaGlyPheValGlnIleCysValAlaValCys	937
Db	2861	GGGAGACCCAGCTCCGCGTGGCCCAAGACGCCCTGGTGGAGGGTGTGTGGCGGACCTGC	2920
QY	938	ArgProGlnHemeIleAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSer	957
Db	2921	TCACCAACTACCGCGCCCTGTACCCAGCGCTTACCTTGTGGACACCACTTCTTAC	2980
QY	958	AspLeuIysProSerArgIlyPrometSerGlyGlyThrGlnValThrIleThrGlyThr	977
Db	2981	CGTGTGAGCCCTCCCTGGGGCCCTGTGCAGGGGGACCTGATGTGGCATTCGAGGGAGC	3040
QY	978	AsnLeuAsnAlaGlySerAsnValValMetPheGlyIysGlnProCysIleuPhe---	996
Db	3041	CACCTGAACGAGGACATGATGTGGCTGTGTGGTGGTGGCGGCGCTCTCTCTCC	3100
QY	997	---HisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGlnValLeu	1015
Db	3101	TGTGTCCAGGAGAACTCCCGTAGATCCGGTGGCTGTGACACCCCGCGGACAGCCCTGC	3160
QY	1016	GlnMetIysValSerValGlnValAspArgAlaIalysIle---HisGlnAspLeuValPhe	1034
Db	3161	AGCGCTCCACATCATCATACATCAACCGCGGCCAGTCCACACCTGTAGGTAACTAC	3220
QY	1035	GlnIysValGlnAspProThrIleValArgIleGlnProGlnTyrPheSerIleValSerGly	1054
Db	3221	AACACACCGAGGAGCCCAACATCTGTAGATGCACCCGAGTGGACATCAACAGCGGT	3280
QY	1055	AsnThrProIleAlaValTPbGlyThrHisIleuAspLeuIleGlnAsnProGlnIleArg	1074
Db	3281	GGGACCCCTCGACGGGTGCACGACCAACCTGCGCACTGGTCGTGAACCCCGAATCCG	3340
QY	1075	AlaIysHisGlyGlyIlySGlnHisIleAsnIleCysGlnValIleuAsnAlaThrGlnMet	1094
Db	3341	GCCAAAGATGAGGACATGAGAGGAGAGAC---TGCTGGGTGTCATATGACACCAACCATG	3397
QY	1095	ThrCysGlnAlaProAlaIleuAlaIleuGlyProAspHisGlnSerAspLeuThrGlnArg	1114
Db	3398	GTAATCCGCGCCCGTGTGGCCCAACCCGTGCGCACGCCACAGACGCTGGGGAGCGG	3457
QY	1115	ProGlnGlnPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnIysThr	1134
Db	3458	CCGATAGAGCGGGGCTTCGTATGAGACACGTCGGCTCCGCTTGTGCTCAATCCAC	3517
QY	1135	AsnPheThrTyrTyrProAsnProValPheGlnAlaPheGlyProSerGlyIleIleuGln	1154
Db	3518	TCTCTCTCTACTACCTCGACCCGCTACTGAGCGACCTACGCCCACTGGCGCTGTGGAG	3577
QY	1155	LeuIysProGlyThrProIleIleLeuIysGlyIysAsnLeuIleProProValAlaGly	1174
Db	3578	CTGAAGCCACCTCCCACTCATCTCTCAAGGGCGGAGAACCTTGGCACT---GCAACC	3634
QY	1175	GlyAsnValIysLeuAsnTyrThrValLeuValGlyGlnIysProCysThrValThrVal	1194
Db	3635	GGCAACTCCCACTCACTACACGAGTGTCTACGTGGCTTCACACCTGTGACCTCACCGTG	3694
QY	1195	SerAspValGlnLeuLeuCysGlySerProAsnLeuIleGlyArgHisIlyValMetAla	1214
Db	3695	TCCGAGACGACACTGCTGTGGAGGCGCCCAACTCTACTGGGAGACAAAGTACCGGTG	3754
QY	1215	ArgValGlyIlyMetGlnTyrSerProGlyMetValTyrIleAlaProAspSerProLeu	1233
Db	3755	CGTGACAGGTGCTTCGAATTCCTCCACAGGACCTGCAGGAGTACTCGGACAGCGCTGTG	3814
QY	1235	SerLeuProAlaIleValSerIleAlaValAlaGlyIlyLeuLeuIleIlePheIleVal	1255
Db	3815	ACGCTGCTGCATTGTGGCATTGGCGAGAGCGGGGGTCTCTGCTGCTGTCATCGTG	3874



1255 AlaValLeuLeuLeuAlaTyrIleValArgIleSerArgIleSerAspLeuThrIleuLeuValArgIleu 1274  
3875 GCTGTGTCTCATCGCTACCAAGCCGCAAGTCAAGAGTGTGACCGCACTCAAGCGGCGG 3934  
1275 GluMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysIleGluAlaPheAla 1294  
3935 CAGGTCAGATGACCAACCTCGAGAGTCCCGGTGGCTCGAATGACAGGAAGCTTTGCA 3994  
1295 GluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGluAlaGlyIleProPhe 1314  
3995 GAGCTGACAGACAGATCCACAGCTGACCAATGACCTGACGAGTCCGCGCATCCCTTC 4054  
1315 LeuAspTyrArgThrTyrThrMetArgValLeuPheProGlyIleGluAspHisProVal 1334  
4055 CTTCATACCGGACATATGCGCATCGGGTCTCTTCTCGGATCGAGACCAACCTGTG 4114  
1335 LeuArgAspLeuGluValProGlyTyrArgGlnGluArgValGluIleGlyLeuVal 1354  
4115 CTCAAGAGATGAGAGTA-----CAGGCCAATGTGAGAGTGTGACACTG 4162  
1355 PheAlaGlnLeuIleAsnAsnValPheLeuLeuSerPheIleArgThrLeuGluSer 1374  
4163 TTCCGGAGCTGTGACCAAGAGCACTTCTGTGATCTTCATCCGACGCTGGAGCA 4222  
1375 GlnArgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeu 1394  
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1395 GlnSerIleLeuGluTyrAlaThrAspValLeuValLeuGlnLeuLeuAlaAspLeuIleAsp 1414  
4283 CAGGCGAGATGAGATACGCCACAGGCTGTCAAGAGCTCTTCTCGACTCATGAG 4342  
1415 LysAsnLeuGlnIleSerIleAsnHisProIleLeuLeuArgArg---ThrgIleSerVal 1433  
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1434 AlaGluIleMetLeuThrAspThrPheThrPheLeuLeuTyrIlePheLeuValGluCys 1453  
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1454 AlaGluIleProLeuPheSerLeuPheCysAlaIleIleGlnIleMetGluValGlyPro 1473  
4463 GCTGGAGGCGCGCTGTATCTCTGATCTGTACGCGCATCAAGACAGAGATGAGAGGCGCC 4522  
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4523 ATTGACGCATCAAGGCGGAGGACGCTACTCTCTGAGTGAAGACAGCTCATCCGCGAG 4582  
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1534 AspAlaIlePheIleAsnValProCysSerHisArgProIleAlaIleAspMetAspLeu 1553  
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1554 GluTyrArgGlnIleSerGlyAlaArgMetIleLeuGlnAspGluAspIleThrThrLys 1573  
4763 GAGTGGCGCGCGCGCGCATGCGCGCTACTCTGACGACGAGGACGACCAACCAAG 4822  
1574 IleGluAsnAspTyrIleValArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySer 1593  
4823 ATTGACACGATTGAGAGAGCTGACACCTGCTGCTACACGAGTGAAGAGCGGTCC 4882  
1594 ValValAlaLeuValSerIleGlnValThrAlaTyrAsnAlaValAsnAsnSerThrVal 1613  
4883 TCGGTGGCACTGTGTCACCAAGACAGCGTCCGCTACCAACTCTCCACTCTCCACTTCC 4942  
1614 SerArgThrSerAlaSerIleTyrGluAsnMetIleArgTyrThrGlySerProAspSer 1633

4943 ACCAAG---TCCCTCAGAGATACGAGAGCATGTGTGCGACGGCGACAGAGCCCGACAGC 4999  
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5000 CTGCGCTCGCCAGCGCCCATGATCAAGCCGACCTGGAGAGCGGACCAACCTGTGAC 5059  
1654 LeuValIleAsnHisGluIleGlyAspGluIleGluIleAspArgIleSerIleMetVal 1673  
5060 CTGCTGAAGAACCAACAGACCACTGACCAAGGCTGAGGTGACCCCGAGGACAAATGTC 5119  
1674 SerGluIleTyrLeuThrArgLeuLeuAlaThrLys---GlyThrLeuGlnIlePheVal 1692  
5120 TCGGAGATCTACTTGAACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5179  
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1752 IleTyrAsnProGlnPheValPheAspIleHisIleAsnSerIleThrAspAlaCysLeu 1771  
5360 ATCAAGAACCCACAGTTGTGTGCTGCACTTCAAGAACACATCAACGAGCTGCTGCTG 5419  
1772 SerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLys 1791  
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1792 AspSerProSerAsnIleLeuLeuTyrAlaIleAspIleProSerTyrIleAsnThrVal 1811  
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1831 AlaTyrLeuAlaGluIleSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeu 1850  
5600 GGTATCTGGCTGAGACATCTCCGCTGACCTGACCGCAGTTCACAGACATGAGCGCTTG 5659  
1851 SerGluIlePheSerTyrValGlyIleTyrSerGluGlu-----IleLeuGlyProLeu 1868  
5660 CACGAGATCTACTCTCAATCAACCAAGTACAGAGTGAAGTGAAGTCTGACGCTG 5719  
1869 AspHisAspAspGluCysGlyIleGlnIleLeuAlaTyrIleLeuGlnIleValIleThr 1888  
5720 GAGAGAGATGACAGAGCGCGCGGCGGAGCGCTCGGACCAAGCTGACAGTGTGAC 5779  
1889 LeuMetSerLeuAspSer 1894  
5780 ACGATGGCCCTGAGCAGC 5797

RESULT 4  
US-09-964-824A-313  
Sequence 313, Application US/09964824A  
Patent No. US20020102531A1  
GENERAL INFORMATION:  
APPLICANT: Horigan, Stephen  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat  
FILE REFERENCE: 689290-73  
CURRENT APPLICATION NUMBER: US/09/964,824A  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US/60/236,033  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US/60/236,032

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; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 313
; LENGTH: 6252
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-03-964-824A-313

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Alignment Scores:	
Pred. No.:	2,66e-268
Score:	2580.00
Percent Similarity:	50.63%
Best Local Similarity:	33.18%
Query Match:	25.83%
DB:	9
Length:	625
Matches:	354
Conservative:	344
Mismatches:	713
Indels:	261
Gaps:	61

US-09-964-956-13 (1-1896) X US-09-964-824A-313 (1-6252)

OY	24	ThrlleuLeuthrArgInlrProLaProleuSerGIuNylGlnAgSerPheValThrpe	43
Db	35	ACCCCTGCTGGGCTGCTGAGCGAGGTGCAGCTGAGAGCCCGGAAAGCTGACCTTCTC	94
OY	44	ArgGIyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle	63
Db	95	CGCAGCGAG-----AAAGAGCTGAACCACTGGCTGTGATGAGAGGCTCAAGCGTGTGTG	148
OY	64	TyrLeuGlyAlaValAsnArgIleTyrIlysLeuSerSerAspLeuValIleuValThr	83
Db	149	TACCTGGGGCGGTGATGCCCTTCAACAGCTGATGGAGAGCTGCAGCTGGAGACAGAG	208
OY	84	HisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIleValGlnThr	103
Db	209	GTCGGCCACGGGCGCCGCGCTGGACAAACAAGAGTGCACGCGCCATCGACAGCCAGCCAG	268
OY	104	CysAsnGluProleuthrThrThrAsnAsnValAsnIysmIleLeuIleTyrIlys	123
Db	269	TGGCATAG---GCTAGATGATGTACAATGTGCACAGCTGCTGTGCTGAGACCTTCCC	325
OY	124	GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu	143
Db	326	AGGAAGCGCTGGTGGAGTGGCGGACGCTTTCAGAGGCAATGTGGCTCTGCGGCGCTG	385
OY	144	GluAsp-----LeuThelysLeuGlyGluProTyrThrIlysllysGlnHisTyrLeuSer	161
Db	386	AGCAACACATCTCCCTCGCGCTGTTCTTACGAGAGCGGACGGGGAGAAATCTTTGTGGCC	445
OY	162	GlyAlaAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAsp	181
Db	446	AGCAATGATGAGGGCGGTGGCCACAGTGGGGCTGTGAGATCCACGGGCTCGTGGTGAC	505
OY	182	LysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrPheProThrHisSerSer	201
Db	506	CGCGTGTGTTGTGGCGAAAGGCATATGGAGCCACAGCAAGCGCATGTGTAGCACT	565
OY	202	ArgLysLeuThrIlysaSerGlnAlaAspGlyMetPheAlaTyrValPheHisAspGlu	221
Db	566	CGGCTGTGGACGGAGTACAGACAGAGGAGGCGTTGAAGCCTTACAGGACAGCAGCAC	625
OY	222	PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp	241
Db	626	TACAAAGCCGGTACCTGTCACCAACAACAAGCACTT-----	664
OY	242	IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro	261
Db	665	-----GTGGGGCGGCTTCGAGAGCGGCGCCCTAGTCTTCTTGTTCACACAG	715
OY	262	GluMetValSerProProGlySerThrThrIlyslGluGlnValTyrThrSerLysLeuVal	281
Db	716	GACAAAG---CACCGGCGCCGAAACCGGACG-----CTGCTGGCA	751

QY 282 ArgLeuCySerIysGluAspThrAlaPheAsnSerIyrValGluValProIleGlyCySerGlu 301  
 Db 752 CGCATGTGCAAGAGAGGCCCACTACTACTCTCTACTGTGAGATGACCTCGACGTCCGG 811  
 QY 302 ArgSerGlyValGluIyrValGLeuLeuGlnAlaIAlaIyrLeuSerIySAAGlyValAlaVal 321  
 Db 812 GACCCCGACATCCAC-----GCCGCTGGCCCTT-----GGCACTCCG 847  
 QY 322 LeuGlyIyrArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerIys 341  
 Db 848 CTGGCCGGCCTCCGTGGGTGGCCGTGGCTGTGGACGGTGTATATGTCTGTCTTACGACGA 907  
 QY 342 GlyGlnIyrsArgIySmetySerLeuAspGluSerAlaLeuCySIIlePheIIleLeuLys 361  
 Db 908 GACAGC-----CGAGCAAGTGGGGGGCCCGGTGGGGCCCTCGCCCTGTCCCGCTGAC 961  
 QY 362 GlnIleAsnAspArgIleIysGluIArgLeuGlnSerCySyrIArgGlyIyGlyIThrLeu 381  
 Db 962 AAGGTGACGCGCAAGATGAGAGGCCAACCGAAGCCTGTATAC-----ACAGCACCCGG 1015  
 QY 382 AspLeuAlaIrrPheLysValIys-----AspIIleProCySerSerAlaLeu 397  
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 QY 398 LeuThrIleAspAspAspAspAspAsp-----CySgIyLeuAsp---MetAlaAlaProLeuGlyVal 415  
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 QY 416 SerAspMetValIArgGlyIleProValPheThrGluAspAspAspAspMetThrSerVal 435  
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 Db 1313 GAGATTAACAAGAGAGTCAAGCGGACCTGTGATCTGTGTGAGACCTGGACGACTGTAC 1372  
 QY 496 IleMetSerGluIArgGlnIleuThrIArgValProIAlaGluSerCySgIyGlnIyGlnSer 515  
 Db 1373 GCCATGACCCGAGCAAGAGTGTTCGGGTGCGGAGGAGAGGTGCTGAGCTTACCCGAC 1433  
 QY 516 CySgIyGlnIyCySLeuGlySerGlyIAspProHisCySgIyIyrCySValIleuHisAsnThr 535  
 Db 1433 TGCACCCAGTGCCTGGACTCCACGAGACCTCTACTGCGGTGCTGCTGCTGAGAGACGA 1492  
 QY 536 CySerThrArgIyrsGluIArgCySgIuIArgSerIyGluProIArgAspPheAla---SerGlu 554  
 Db 1493 TGCACCCGGAAGGCCAGAGTGTCCGGGGCCAGAGAGGCCAACCACTGCTGTGAGCCGA 1555  
 QY 555 MetIySgIyCySValIArgLeuThr---ValHisProAsnAsnIleSer---ValSerGln 572  
 Db 1553 AGCAAGTCTCTGATGGCGGTCAACGACGCCACGACCAAGAACTATGACGGCGGCGCCAG 1612  
 QY 573 TyrAsnValIleuLeuValLeuGlnIThrIyrAsnValProIuLeuSerAla-----Gly 590  
 Db 1613 GGGAGGTGACAGCTGACCTCAGCCCC-----CTCCCTGGCCTGAGCGAGAGACGAG 1666  
 QY 591 ValAsnCySThrPheGluAspLeuSerGluMetAspGlyLeuValIyGlyAsnGlnIle 610  
 Db 1667 TTGCTGTGCTTTTGGGAGGTGGCGCCGACACACCCCGCGCTGAGAGGCGACGGCGTC 1722  
 QY 611 GlnCySyrIyrSerProAlaIySgIyValProIArgIleIleThrGluAsnGly---Asp 629  
 Db 1727 ATCTGCAACTCCCAAGAC-----ATCCCC-----GTCAACCGCGACGCGACGAC 1777  
 QY 630 HisHisValIValGlnLeuGlnLeuLysSerIySgIuIyMetThrPheAlaSerThr 649

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Db 1775 CAGGTGGCCGGACCATCCAGCTCTCTTACAGAGCAACATCTTCTCAGCTCTAC 1834
Qy 650 SerPheValIleuThrLeuProCysLeuHisAsnSer-----CysLeu 663
Db 1835 CAGTACCCCTTCTTACGACTGCGCCGAGCCCATGAGGAGAGAACTCCCGCTGATC 1894
Qy 664 SerCysValIleuSerProTyrArgCysHisIleTyrCysLeuTyrArgHisValCysThrHis 683
Db 1895 TCCTGCGGTGAGCAACCGCTGACTGCGCAGTGGAGCTGCGTACACGAGTGCCTGGAG 1954
Qy 684 ---AspProIysThrCysSerPheGlnGluGly-----ArgValIleuProGluAsp 700
Db 1955 GCTTGGCCCAACCT-----GAGAGCGGCTGCTGCTGCGCCACATGAGAGAGAGC 2005
Qy 701 CysProGlnIleuLeuArgValAspIleLeuValProValIleuValIleuLysProIle 720
Db 2006 TGTCCCAAGTCTCTCGGAGCCAGCCCGCTGCTGATCCCATGAAACGAGAGATGTC 2065
Qy 721 ThrLeuLysAlaIleuAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIle 740
Db 2066 AACTTCCAGGCAAGAACTCTGAC-----2089
Qy 741 LeuAsnIleGlnIleuSerGlnGluArgValProIle-----LeuArgPheAsnSer 758
Db 2090 ---ACCGTGAAGGTTCTCTCTCTGACGTGGGAGTACTGCTGCTCAAGTTCATGAGCCG 2146
Qy 759 SerValGlnCysGlnAsnThrSerTyrSerTyrGlnIleuMetGluIleAsnAsn-----776
Db 2147 GTGACCATGACGATCTGAGGACCTTCTGCGACCCCAAGCTGCTCCAGATGCG 2206
Qy 777 -----LeuProValGluLeuThrValValTyrAsnGlnHisPheAsnIleAspAsn 793
Db 2207 AACGAGACGCTGCTGCTGACCTTACGTCAAGTCTTACGCAAG---AATATTCAGC---2260
Qy 794 ProIleAsnLeuLysValHis-----LeuTyrLysCysGlyAlaMetArgGluSerCys 811
Db 2261 ---AGCAAGCTCATGTGACCTCTACCAACTGCTCTTGGCCCGCAGCGATGCG 2311
Qy 812 GlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTyrCysGlnIleProGlyGln 831
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Qy 832 CysThrLeuArgGlnHisCysProIleGlnIleuSerGlnIleuProIleValAla 851
Db 2372 TGGGTGTAGAGGCCCTGTGC-----AACACC 2398
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Db 2399 AACTCCGAGTCCCGCCCGCTGATCCAGAGATCCAGCTGAGAGCGCGCCCTGGGT 2458
Qy 872 GlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAla 891
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Qy 892 SerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAla 911
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Qy 932 IleCysValAlaValCysArgProGluPhe-----MetAlaArgSerSer-----946
Db 2633 GTGAGCGTC-----TTCCGGAACCTGGCGCTTCCCTCCCAATGTC 2674
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Db 2675 CAGTTCACTTCCAAACAGCCCAAGCTCTCACT---GTGAGAGCCGACGACGAGCCGAG 2731
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Qy 1007 AsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnValAspArgAla 1026
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Qy 1075 AlaLysHisGlyGlyLysGlnHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 1094
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Qy 1095 ThrCysGlnAla-----ProAlaLeuAlaLeuGlyProAspHis-----1107
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Qy 1108 -----GlnSerAspLeuThrGluArgProGluGluPheGly 1119
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Qy 1120 PheIle-----LeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsn 1135
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Db 3275 TTCGAGTACGTCCTGACCCCACTTGAAGAACTTC-----3310
Qy 1156 LysProGlyThrProIleIleLeuLysGlyAsnLeuIleProProValAlaGlyGly 1175
Db 3311 ---ACAGTGGCGTCAAGAGACGTCACAAAGCTCATTCACAGCCCGGGGACCC 3361
Qy 1176 AsnValLysLeuAsnTyrThrVal-----LeuValGlyLysProCys 1190
Db 3362 AATCTGAACAAGCGATAGCGTGCAGAGAGCCGAGCCTTGTGGTGGCGAGCGCTGC 3421
Qy 1191 ThrVal---ThrValSerAspValAlaLeuLeuCysGlySerProAsnLeuIleGlyArg 1209
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Qy 1210 HisLys-----ValMetAlaArgVal 1216
Db 3482 CCCAGCGCGCGGAGAAAGACACACACACAACTGCCGAGTTCATTTGAAGTTC 3541
Qy 1217 GlyGlyMetGluTyrSerProGlyMetValTyrIle-----AlaProAspSerPro 1233
Db 3542 GGCTCTCGAGAGTGGTGTGCGCGCGGTGAGTACGACACAGCGGTAGCGACCTGCCG 3601
Qy 1234 LeuSerLeu-----ProAlaIleValSerIleAlaValAlaGly 1246
Db 3602 CTCAGCTCATCTTGGCGGTGTGATCGGCCCAAGTGTGTGATCGCGGTGCT---3658
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Db 3659 -----GCTCACTGCTACTGAGAGAGAGCCAGCGAG 3688
Qy 1267 SerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAla 1286
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QY	128	LeuGluCysArgSerGluIlePheAlaLeuGlnIleThrAspIleIleGluLeuThrSerAsp	1306
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QY	1307	LeuAspGluValaGlyIleProPheLeuAspTyrArgThrTyrThrMetArgValLeuPhe	1326
Db	3809	GTGCACAGAGCGCGGCATCCCGTGGCTGGACTTACAGACCTTACACCGACCGGCTTCTTC	3868
QY	1327	-----ProGlyIleGluAspHisPheValLeuArgAspLeuGluValProGly	1342
Db	3869	CTGCCTCCCAAGACCGCGACAGAGAGTATGATACCGGCAAGCTGGACATCCCTGGAG	3928
QY	1343	TyrArgGlnGluArgValGluValSerGlyLeuValLeuPheAlaGlnLeuIleAsnValLys	1362
Db	3929	CCGGGGGGCGCGGTGGTGGAGCAGCGCCCTTACAGTTCACACTGCTGAAACAGAGAG	3988
QY	1363	ValPheLeuLeuSerPheIleArgThrLeuGlnSerGlnArgSerPheSerMetArgAsp	1382
Db	3989	TCTTCTCATCATTTTCATTCACACCTGGAGAACCGAGGGAGTCTCGGCGCGCGCC	4048
QY	1383	ArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyrAlaLeu	1402
Db	4049	AAGGTCTACTTGGGTCCCTGGCTTACCGGTGGACCGGAAACTGGAGTCACTACG	4108
QY	1403	AspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGlnSerLysAsnHis	1422
Db	4109	GACATCTGACACAGCTTCTCTGGAGCTCTGGAGCAGTACGAGTGGCGCAAGAAC--	4165
QY	1423	ProLysLeuLeuLeuLeuArgThrGlnSerValAlaGluLysMetLeuThrAsnThrPhe	1442
Db	4166	CCCAAGCTGAGCTGCGGAGGTCTGAGCTGTGGTGGAGAGAGTCTGCTCCACTGGATG	4225
QY	1443	ThrPheLeuLeuTyrLysPheLeuLysGlnLysCysAlaGlyLeuProLeuPheSerLeuPhe	1462
Db	4226	TCCATCTGCTGTGACACAGTACTTCAAGACAGCTGCCGGGAGCCCTGTACAGCTCTTC	4285
QY	1463	CysAlaIleLysGlnGlnMetGlnLysGlyProIleAspAlaIleThrGlyAlaLys	1482
Db	4286	AAGGCATCAAAACATCAGGTGAAAGAGGCCCGGTGATGCGGTACAGAAAGAGCCAG	4345
QY	1483	TyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLysThrLeuValLeu	1502
Db	4346	TACACTCTCAACGACACGCGGCTGTGGGGGATGATGTGGAGTACGCAACCCCTGACCGTG	4405
QY	1503	SerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCys	1522
Db	4406	AGCGTGAATCTGCAGAGACGAG--GGAATGAGCGCATCCCGGTGAAGTCTCTCAATGT	4462
QY	1523	AspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsnValProCys	1542
Db	4463	GACACCATCTCCACAGTCAGAGAGAAAGTCAATTGACGGGTGACCGGTGGACCCCTGC	4522
QY	1543	SerHisArgProLysValAlaAspMetAspLeuGlnTyrPARGlnGlnLysSerGlyAlaArg	1562
Db	4522	TCTTGCTGGCCAGGCGCACAGCGCTGTGCTGAGTGGGCTCGGCGGTCCACAGCGGAG	4582
QY	1563	MetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTyrLysArgLeuAsn	1582
Db	4583	---ATCCTGTCCGACTCGGACTGTGACGTGACGACCGGAGGGCGGTGGAAACGGGTCAAC	4639
QY	1583	ThrLeuAlaHisTyrGlnValProAspGlySerValAlaAlaLeuValSerLysGlnVal	1602
Db	4640	ACCCATTAGCATTAAGATCGGGATGGAGCCATCCATCCTG-----	4684
QY	1603	ThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrGlu	1622
Db	4685	-----TCCAAAGTGGGGGTCTCCACGACCGGAGAGACACCGACGAG	4726
QY	1623	AsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMetIleThr	1642
Db	4727	GACCTG-----CCTGGGGAGGCCCATGCGCTC-----	4753

```

QY      1643  Prokshpseugiussergilyvalylvsmettrpshileuvallyasasnhi:sgluhi:sglyasp 1662
Db      4754  -----CTGAGAGAGAGGAACCCGGGTGTGGCACTGTGTGGCGCCGACCGACGACGAGGTGGAC 4807
QY      1663  Glnlysgluuglyasparglyser-----lysmetvalserglu 1675
Db      4808  GAGGGCAAGTCCAAAGAGAGGCAAGCGGTGAAAGAGAGAGCGGACGAGGCAAGGCCATACCGAG 4867
QY      1676  Ilertryleuthrargyleuleuvalathetysgllythirleuglnlysphevalaspdieu 1695
Db      4868  ATCTACCTGACGCGCGCTCTCTCTCAAGGCAACATCGACGAGCTTGTGGACAACCTTC 4927
QY      1696  Pheglutthrlpheaserthrallhiargglyseralaleuproleualalilelystyr 1715
Db      4928  TTCGACAGCGGTCGGCGCCCTGGGCAC-----GCGGTCGCACTCGACGTCAAGTAC 4978
QY      1716  Metpheasppheleuasprgluglnalasparyshisgilylehi:asp:prohi:eva:arg 1735
Db      4979  TCTTCGACTTCCTCGAGAGACGACGAGGAGAGACAAATCCAGATGAGACACCATC 5038
QY      1736  Histhrtrplysaserahenysleuproleuargphetrpvalaammetileysasp:pro 1755
Db      5039  CACATCTCGAAGAGACGACGCTTCACCGTCCGGTTCGGGTGAACATCTCCAGAACCC 5098
QY      1756  Glnphevalpheaspi:lehi:ely:asnsertilethraspalacylseser:val:val:ala 1775
Db      5099  CACTTCATCTTTGACGTGCATGTCACAGAGGTGGTGGACGCGCTGCATGTCATCCG 5158
QY      1776  Glnthrpheleaspserser:cyser:thser:glunhi:sargleuuglylyasps:proser 1795
Db      5159  CAGACTTCATGAGAGCGCTTCGACGCGGACGAGGACATTAAGCGCGGATTCCTCCAC 5218
QY      1796  Asnlysleuleu:lyz:al:al:ysasp:ile:proser:tyr:lys:asn:trp:val:glu:arg:tyr 1815
Db      5219  AACAAGCTGCTGTACGCCAAGAGATCTCCACCTACAGAAAGATGTGAGAGATTACTAC 5278
QY      1816  Seraspilleglylysmet:proal:aleser:asprglnasmet:asn:al:aty:leu:al:glu 1833
Db      5279  AAGGGAGATCCGGCAATAGTGTGCAAGGTCCAGCCACGACGACATGAAACACACCTGGCAAG 5338
QY      1836  Glnserargmet:hi:met:asn:glu:phes:anthr:met:ser:al:aleu:ser:glu:ile:pheser 1855
Db      5339  ATTTCGGGGGGGCAACGAGATCCTTTGAACACCTCGGGACATCCACAGCTTCAACA 5396
QY      1856  Tyrval:gllylystyserserglun:ile:leu:gl:pro:leu:asph:laspp:glu:ty:sgly 1875
Db      5399  TACACGACGAAATACTATGACCAAGATCAATCAATGCTCTTGAGAGAGATCTCGCCGCCAG 5455
QY      1876  Lysglnlysleualaty:tyr:lys:leu:glu:lnval 1886
Db      5459  AAGATGCACTGCGCTTCGCGCTCGGCTCGACGAGATT 5491

RESULT 5
US-09-930-213-254
US-09-930-213-254, Application US/09930213
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ANDRE
APPLICANT: HINZMANN, BERND
APPLICANT: SCHAFER, REINHARD
APPLICANT: ZUBER, JOHANNES
APPLICANT: TCHÉ-NITSE, OLEG
APPLICANT: GRIPS, MARTIN
APPLICANT: HELLMGEL, MARTIN
APPLICANT: SCHMITZ, ANNE-CHANTAL
APPLICANT: SERS, CHRISTINE
TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
FILE REFERENCE: ALBRE-14
CURRENT APPLICATION NUMBER: US/09/930,213
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: DE 10004102.7
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 885

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SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 254  
 LENGTH: 6252  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-930-213-254

## Alignment Scores:

	2.66e-268	Length:	6252
Pred. No.:	2580.00	Matches:	654
Score:	50.63%	Conservative:	344
Percent Similarity:	50.63%	Mismatches:	713
Best Local Similarity:	33.18%	Indels:	260
Query Match:	25.83%	Gaps:	61

US-09-964-956-13 (1-1896) x US-09-930-213-254 (1-6252)

QY 24 ThrLeuLeuThrArgGlnProAlaProLeuSerGlnArgSerPheValThrPhe 43  
 DB ACCCTGCTGGCGCTGCGGCGCAGGTGCCAGCTGAGCCGCCCAAGCTGACTTCTTC 94  
 QY 44 ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle 63  
 DB CCCAGCGAG-----AAAGAGCTGAACCACTGCTGTGATGAGGCTCAGCGCTG 148  
 QY 64 TyrLeuGlyAlaValAlaAsnArgIleTyrIleuSerSerAspLeuIleuValThr 83  
 DB TACCTGGGGGGCGGTGATGCTTACCAAGCTGATGCAAGCTGCACTGAGCAGCAG 208  
 QY 84 HisGluThrGlyProAspGluAspAsnProIleCysTyrProProArgIleValGlnThr 103  
 DB GTGGCCACCGGCGCGCGCTGAGCAACAGAGTCCAGCGCGCCATGAGGCCAGCCAG 268  
 QY 104 CysAsnGluProLeuThrThrAsnAsnValAsnIleuMetLeuLeuIleAspTyrIle 123  
 DB TCCCATGAG-----GCTGAGATGACTGACATGTCACCAAGCTGCTGCTGCACTGCC 325  
 QY 124 GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysIleLeuLeuArgIle 143  
 DB AGAAGCGCGCTGAGTGGAGTGGCGAGCGCTTCAAGGGGAGTCTGCTGCGCGCGCTG 385  
 QY 144 GluAsp-----LeuPheIleuGlyGlnProTyrHisIleValGluHisIleTyrLeuSer 161  
 DB AGCAATATCTCCCTCCGCTGTTTACAGAGAGCGGAGCGGAGAGATCTTGGTGGCC 445  
 QY 162 GlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 181  
 DB AGCAATGATGAGGCGCTGGCCACAGTGGGCTGTGAGCTCCACGCGTCTGGTGTAC 505  
 QY 182 LysLeuPheIleIleThrAlaValAlaAspGlyLysProGluTyrPheProThrIleSerSer 201  
 DB CGGCTGCTGTTTGGGCAAGGCAATGGGCCACACAGACGACATCATCTGAGCACT 565  
 QY 202 ArgIleLeuThrLysAsnSerGlyAlaAspGlyMetPheAlaTyrValPheHisAspGlu 221  
 DB CGGCTGTTGACCGGACTGACAGCAGCAGGAGGCTTGAAGCTTACCGACCGACCCACC 625  
 QY 222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241  
 DB TACAAAGCGCGCTGCTGTCACCAACACACAGCACTC----- 664  
 QY 242 IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro 261  
 DB GTGGCGGCTTCCGAGGAGCGGCGCTGCTGCTTCTTCTTCAACACAGCAG 715  
 QY 262 GluMetValSerProProGlySerThrThrIleGluGlnValTyrThrSerIleVal 281  
 DB GACAAAG--CACCCGCGCGGAGCCGACG-----CTGCTGGGA 751  
 QY 282 ArgLeuCysIleGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCysGlu 301  
 DB CGCATGTGACAGAGAACCCCACTACTACTCTGAGATGAGATGAGCTGAGTGC 811

QY 302 ArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerIleValGlyAlaVal 321  
 DB GACCCCGACATCCAC-----GCCGTGCTT-----GGCACCTGC 847  
 QY 322 LeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerIle 341  
 DB CTGGCGGCTCGGTGAGTGGCGCTGCTGCGAGGGGTATATGCTGCTTCCAGCA 907  
 QY 342 GlyIleuArgIleMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuIle 361  
 DB GACAGC-----CGAGCAGATGGGGGGCGCGCGGCTGCTGCTGCTGCTGCTGAC 961  
 QY 362 GlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeu 381  
 DB AAGGTGACCGCAGAGATGAGGCCAACCGCAAGCTGTAC-----ACAGCACCGCG 1015  
 QY 382 AspLeuAlaTrpLeuIleValIle-----AspIleProCysSerSerAlaLeu 397  
 DB GAGCGCGTGAATCTTCTTCAAGCCCTTCCACGGCGATATCACTGCGCGCGCACGG 1075  
 QY 398 LeuThrIleAspAspAsnPhe--CysGlyLeuAsp--MetAsnAlaProLeuGlyVal 415  
 DB CCGGCTCCAGACAGACTTCCCATGTGCTGCGAGCACCTGCTTACCCGCTGAGCAGC 1135  
 QY 416 SerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVal 435  
 DB CGGACGAGGCTGAGAGGACAGCCGCTGCTGACGCTGAGAGGCTGACCTCAGCGCGCT 1195  
 QY 436 IleAlaTyrValTyrIleAsnHisSerLeuAlaPheValGlyThrLysSerGlyIle 455  
 DB ACCGTGCGCGCGAGAACCAACCACTGTGCTTCTTCTGAGACCTCTGANTGCGCGAG 1255  
 QY 456 LysIleIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal 475  
 DB CTCAAGGTGACTTACC--CCAGTGGACCTCTCAGAGTACAGACTTCTCCTG 1312  
 QY 476 ValAspProGlyProValIleuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyr 495  
 DB GAGATTAACAAAGAGTCAAGCGGACCTGTACTGTGAGACCTGCGAGCGCTGTAC 1372  
 QY 496 IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer 515  
 DB GCCATGACCCAGGACAGAGTGTCCGCTGCGAGTCCAGAGAGTCTGAGCTACACCGGAC 1432  
 QY 516 CysGlyIleCysLeuGlySerGlyAspProHisCysGlyTyrCysValIleuHisAsnThr 535  
 DB TGCACCCAGTCCCGGACTCCAGAGACCTTACTGCGGCTGCGTCCGAGGAGCA 1492  
 QY 536 CysThrArgIleGluArgCysGlyIleArgSerIleGluProArgArgPheAla--SerGlu 554  
 DB TGCACCCAGTCCCGGACTCCAGAGACCTTACTGCGGCTGCGTCCGAGGAGCA 1552  
 QY 555 MetLysGlnCysValArgLeuThr--ValHisProAsnAsnIleSer--ValSerGln 572  
 DB AGCAAGTCTGCTGCGGCGGCTGACAGCGCCACCAAGACATGAGCGCGGCGGAC 1612  
 QY 573 TyrAsnValLeuLeuValIleuGluTyrTyrAsnValProGluLeuSerAla-----Gly 590  
 DB GGGAGGCTGAGCTGACCGTCCAGCCG-----CTCCCTGCTGAGCGAGAGAGAG 1666  
 QY 591 ValAsnGlyAsnThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610  
 DB TTGCTGTGCTTCTTGGGAGTGGCGCGGACACCCCGCGCGTGGAGGCGAGGCGCTG 1726  
 QY 611 GlnCysTyrSerProAlaAlaIleGlyValProArgIleIleThrGluAsnGly--Asp 629  
 DB ATCTGCAACTCCCAACAGC-----ATCCCC-----GTCAACCGCAGCGAGGAC 1774  
 QY 630 HisHisValValGluLeuGlnLeuLysSerIleGluThrGlyMetThrPheAlaSerThr 649  
 DB CAGGTGCGGTGACCATTCAGCTCTCTTACAGACAGCAACATCTTCTCAGCTCTAC 1834  
 QY 650 SerPheValPheTyrAsnCysSerValHisAsnSer-----CysLeu 663







US-09-964-956-13 (1-1896) x US-10-108-260A-802 (1-3666)

QY 1510 AlaAsnSerProGluValProValLysIleLeuAsnCyAspThrIleThrGlnValLys 1529

DB 2 GCCAACAGCCCGAGAGTCCAGTAAGATCCTCAAGTGTGACCATCAGCATCAGCTCAGGCAAG 61

QY 1530 GluLysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaAla 1549

DB 62 GAGAGATTTCTGAGATGCCATCTTCAAGATGTGCTTCTCCACCGGCCCAAGGCTGCA 121

QY 1550 AspMetAspLeuGluTTPArgGlnGlySerGlyValAspMetIleLeuGlnAspGluAsp 1569

DB 122 GATATGATCTGTGATGGGACAGAGAAAGTGGGGACAGAGATGATCTTGACAGATGAAGAC 181

QY 1570 IleThrThrLysIleGluAsnAspThrLysArgLeuAsnThrLeuAlaHisTyrGlnVal 1589

DB 182 ATGACACCAAGATGAGATGATGAGAGAGCACTGAAACACCTGGCCCACTACAGGTG 241

QY 1590 ProAspGlySerValValAlaLeuValSerLysGlnValIThrAlaTyrAsnAlaValAsn 1609

DB 242 CCAGATGTTCCGTGGTGGCATTTAGTGTCAAGCAGGTGACAGCTTATAAGCAGTGAAC 301

QY 1610 AsnSerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGly 1629

DB 302 AACTCACCGTCCAGAGACCTCAGCAAGTAAATGAAACATATATCGGTACCGGGGC 361

QY 1630 SerProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyVal 1649

DB 362 AACCCCGAGAGCTCCGCTCAGCAGCACTAGATGACCTCGACCTGGAGAGTGAATC 421

QY 1650 LysMetTTPHisLeuValLysAsnHisGluHisGlyAspGlnLysGluLysAspArgGly 1669

DB 422 AAGATGTGCACCTAGTGAAGAACCAAGCAGCAGGAGCAAGAAAGAGGGAGCCGGGG 481

QY 1670 SerLysMetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGln 1689

DB 482 AGCAAGATGTGTCTGAATCTTACCTGACCCCACTCTGGCCACTAAGGGCACTGAG 541

QY 1690 LysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeu 1709

DB 542 AAGTTGTGATGATGATCTTTGAGACCATCTTCAGACGGCAGCCGTCCTGCTGCTG 601

QY 1710 ProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyLe 1729

DB 602 CCCCTGGCATCAAGTACATGTTGACTTCTGATGACGAGGCTGATTAACATGGCAAT 661

QY 1730 HisAspProHisValArgHisThrTyrLysSerAsnCyLeuProLeuArgPheTyrVal 1749

DB 662 CATGACCCGACGCTCGCCATACCTGGAAGAGCAATGCTGCCCTGAGGTTGGGTC 721

QY 1750 AsnMetIleLysAsnProGlnPheValIlePheAspIleHisLysAsnSerIleThrAspAla 1769

DB 722 AACATATCAAGAACCCGAGTTGTGTTGATTCATCAAAAGCAAGCATCAAGACGCC 781

QY 1770 CysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeu 1789

DB 782 TGCTCTCTGTGTGTGCTGAGACCTTCATGACTCTGCTCCACGTCAGAGCAGCGGCTG 841

QY 1790 GlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsn 1809

DB 842 GGGAGAGAGACTCGCCCTCAACAGAGCTGTATGCCAAGAGATCCCGCAGTCAAGAGAT 901

QY 1810 TTPValGluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMet 1829

DB 902 TGCGTGAAGAGATTAATCAAGCATAGGAGAGATGCCAGCATCAAGCAGCAAGCATG 961

QY 1830 AsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAla 1849

DB 962 AACGCAATACCTGCTGAGAGCTCCCGATGCAATGAAGATTCACCAACCTGAGTGA 1021

QY 1850 LeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIleLeuGlyProLeuAsp 1869

DB 1022 CTCTCAGAGATCTTCTCTATGTGGCAATATACAGGAGAGATCTCTGACCTTGAC 1081

QY 1870 HisAspAspGluCysGlyLysGlnLysLeuAlaTyrLysLeuGluGlnValIleThrLeu 1889

DB 1082 CAGCAGCAGCAGGTGTGGAGAGAGCAAGAACTGGGCTCAAACTGAACATGATAACCTTC 1141

QY 1890 MetSerLeuAspSer 1894

DB 1142 ATGAGCTTAGACAGC 1156

RESULT 7

US-10-245-103-91

/ Sequence 91, Application US/10245103

/ Publication No. US20030068778A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin

/ APPLICANT: Baton, Dan

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Guiney, Austin

/ APPLICANT: Smith, Victoria

/ APPLICANT: Stephan, Jean-Philippe

/ APPLICANT: Matambe, Colin

/ APPLICANT: Wood, William

/ APPLICANT: Zhang, Zemin

/ APPLICANT: Fong, Sherman

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P3630R1C112

/ CURRENT APPLICATION NUMBER: US/10/245,103

/ PRIOR FILING DATE: 2002-09-17

/ PRIOR APPLICATION NUMBER: 10/197942

/ PRIOR FILING DATE: 2002-07-18

/ PRIOR APPLICATION NUMBER: 60/059114

/ PRIOR FILING DATE: 1997-09-17

/ PRIOR APPLICATION NUMBER: 60/063046

/ PRIOR FILING DATE: 1997-10-24

/ PRIOR APPLICATION NUMBER: 60/065027

/ PRIOR FILING DATE: 1997-11-10

/ PRIOR APPLICATION NUMBER: 60/079689

/ PRIOR FILING DATE: 1998-03-27

/ PRIOR APPLICATION NUMBER: 60/086478

/ PRIOR FILING DATE: 1998-05-22

/ PRIOR APPLICATION NUMBER: 60/087607

/ PRIOR FILING DATE: 1998-06-02

/ PRIOR APPLICATION NUMBER: 60/089801

/ PRIOR FILING DATE: 1998-06-18

/ PRIOR APPLICATION NUMBER: 60/090557

/ PRIOR FILING DATE: 1998-06-24

/ PRIOR APPLICATION NUMBER: 60/090689

/ PRIOR FILING DATE: 1998-06-25

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 116

/ SEQ ID NO 91

/ LENGTH: 2597

/ TYPE: DNA

/ ORGANISM: Homo Sapien

US-10-245-103-91

Alignment Scores:

Pred. No.: 1.06e-137 Length: 2597

Score: 1372.00 Matches: 264

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.62% Mismatches: 0

Query Match: 13.73% Indels: 0

Gaps: 0

US-09-964-956-13 (1-1896) x US-10-245-103-91 (1-2597)

QY 194 GluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMet 213

DB 2 GAGTATTTTCCACCACTCTCAGCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATG 61



QY 214 PheAlaTyrValPheHisAspGluPheValAlaSerMetIleLeuSileProSerAspThr 233  
DB 62 TTGGGATACGCTTCCATGATGAGTGGCTGCTCCATGATTAGATCCCTTCGACACC 121  
QY 234 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAspPhe 253  
DB 122 TTCACCATCATCCCTGACTTGATATCTACTAGTCTTAGGTTTAGAGTGGCACTTT 181  
QY 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThrLeuGlu 273  
DB 182 GTCTACTTTTGACCTCCACCTGAGATGGTGTCTCCACAGGCTCCACACCAAGAG 241  
QY 274 GlnValTyrThrSerLeuValArgLeuGlyGlyGluAspThrAlaPheAsnSerTyr 293  
DB 242 CAGGTGTATACATCCAAAGCTCGTGGCTTGGCAAGAGGACACAGCTTCACTCTAT 301  
QY 294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuGlnAlaAla 313  
DB 302 GTAGAGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTCAGAGCTGCC 361  
QY 314 TyrLeuSerLeuAlaGlyAlaValIleuGlyArgThrLeuGlyValHisProAspAsp 333  
DB 362 TACTGTCCAAAGCGGGGCGCTGCTGGACAGACCTTGGAGTCCATCCAGATGATGAC 421  
QY 334 LeuLeuPheThrValPheSerTyrGlyGlnLysArgLysMetLysSerLeuAspGluSer 353  
DB 422 CTGCTCTTCAACCGCTTCTCCAAAGGCCAGAAAGGAAATGAAATCCCTGGATGATCG 481  
QY 354 AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer 373  
DB 482 GCCCTGTGATCTTTCATCTTGAAGCAGATAATGACCCCATTAAGAGACGGCTGACATCG 541  
QY 374 CysTyrArgGlyGlyGluTyrThrLeuAspLeuAlaTyrPheLysValLysAspIleProCys 393  
DB 542 TGTATCCGGGGCGAGGGCACGCTGAGCGCTGAGCTGCTCAGAGTAAAGACATCCCTGCG 601  
QY 394 SerSerAlaLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetAsnAlaProLeu 413  
DB 602 AGCAGTGGGCTCTTACCATGATGACGATGATCTTCTGGGCTGACATGAAATGCTCCCTG 661  
QY 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr 433  
DB 662 GAGGTGTCCGACATGTGTGGTGAATCCCGTCTTCAGAGACAGAGGACCGCATGACG 721  
QY 434 SerValIleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGly 453  
DB 722 TCTGTATCGCATATCTCAAAAGACCATCTCTGCGCTTGTGGGACCAAAAGTGGC 781  
QY 454 LysLeuLysLysTle 458  
DB 782 AAGCTGAAGAGAGGTG 796

RESULT 8  
US-10-245-107-91  
Sequence 91, Application US/10245107  
Publication No. US20030068779A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eator, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C71

CURRENT APPLICATION NUMBER: US/10/245,107  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Number of Prior Application data removed - See File Wrapper or PALM.  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-107-91

Alignment Scores:  
Pred: 1.06e-137 Length: 2597  
Score: 1372.00 Matches: 264  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.62% Mismatches: 0  
Query Match: 13.73% Indels: 0  
Gaps: 0  
DB:

US-09-964-956-13 (1-1896) x US-10-245-107-91 (1-2597)

QY 194 GluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMet 213  
DB 2 GAGATTTTCCCAACCATCTCCAGCCGAAACTGACCAAGAACCTGAGGCGATGGCAGAC 61  
QY 214 PheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr 233  
DB 62 TTGGGATACGCTTCCATGATGAGTGGCTGCTCCATGATTAGATCCCTTCGACACC 121  
QY 234 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAspPhe 253  
DB 122 TTCACCATCATCCCTGACTTGATATCTACTAGTCTTAGGTTTAGAGTGGCACTTT 181  
QY 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThrLeuGlu 273  
DB 182 GTCTACTTTTGACCTCCACCTGAGATGGTGTCTCCACAGGCTCCACACCAAGAG 241  
QY 274 GlnValTyrThrSerLeuValArgLeuGlyGlyGluAspThrAlaPheAsnSerTyr 293  
DB 242 CAGGTGTATACATCCAAAGCTCGTGGCTTGGCAAGAGGACACAGCTTCACTCTAT 301  
QY 294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuGlnAlaAla 313  
DB 302 GTAGAGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTCAGAGCTGCC 361  
QY 314 TyrLeuSerLysAlaGlyAlaValIleuGlyArgThrLeuGlyValHisProAspAsp 333  
DB 362 TACTGTCCAAAGCGGGGCGCTGCTGGACAGACCTTGGAGTCCATCCAGATGATGAC 421  
QY 334 LeuLeuPheThrValPheSerTyrGlyGlnLysArgLysMetLysSerLeuAspGluSer 353  
DB 422 CTGCTCTTCAACCGCTTCTCCAAAGGCCAGAAAGGAAATGAAATCCCTGGATGATCG 481  
QY 354 AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer 373

```

Db      482 GGCCTGTGATCTTCTTCACTTGAAGCAGATTAATGACCGCATTTAGAGCGGCTGCAGTCT 541
Qy      374 CysTYrARgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys 393
Db      542 TGTACCGGGGCGACGGGCGACGCTGACCTGGCTGGCTGAAGGATCAATCCCTCCG 601
Qy      394 SerSerAlaLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetSerAlaProLeu 413
Db      602 AGCAGTGGCTCTTAAACCATTAACGATACCTTGCTGGCTGACATGAATGCTCCCTG 661
Qy      414 GluValSerAspMetValARgGlyIleProValPheThrGluAspArgAspArgMetThr 433
Db      662 GGAATGTCACATGATGAGCTGATTCCTGCTTCAAGGAGACAGGAGCGGATGAG 721
Qy      434 SerValIleAlaIleValIleValAsnHisSerLeuAlaPheValGlyThrLysSerGly 453
Db      722 TCTGTATCCCATATGTCTCAAGAACCACTCTGCTTGTGGGCAACAAAGTGGC 781
Qy      454 LysLeuLysLysIle 458
Db      782 AACCTGAAGAGGTG 796

RESULT 9
US-10-245-143-91
; Sequence 91, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-143-91

```

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Alignment Scores:
Pred. No.: 1,056-137 Length: 2597
Score: 1372.00 Matches: 264
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.62% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 14 Gaps: 0

US-09-964-956-13 (1-1896) x US-10-245-143-91 (1-2597)
Qy      194 GluTYrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMet 213
Db      2 GAGATATTTCCACCATTCACGCGGAACTGACCAAGACTTGAAGCGGATGCG 61
Qy      214 PheAlaTYrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr 233
Db      62 TTCGGCTAGCTCTTCATGATGATGAGTGGCTGCTGATGATTAGATCCCTTCGACACC 121
Qy      234 PheThrIleIleProAspPheAspIleTYrTYrValTYrGlyPheSerSerGlyAsnPhe 253
Db      122 TTCACCATCATCCCTGACTTGATATCTATATGATGATGATTTAGCATGGCACTTT 181
Qy      254 ValTYrPheLeuThrLeuGluProGluMetValSerProProGlySerThrThrLysGlu 273
Db      182 GTCTACTTTTGAACCTTCACACCTGAGATGATGTGTCTCCACCAAGCTCCACCAAGAG 241
Qy      274 GluValIleTYrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTYr 293
Db      242 CAGGTGTATACATCCAAAGCTGCTGAGGCTTGGACAGGACACAGCTTCACTCAT 301
Qy      294 ValGluValProIleGlyCysGluArgSerGlyValGluTYrArgLeuGluAlaAla 313
Db      302 GTAGAGTGCCCATTCCTGCTGAGGCGACGTGGGTGAGTACCGCTCTCGACGCTGCC 361
Qy      314 TYrLeuSerLysAlaGlyAlaValleuGlyArgThrLeuGlyValHisProAspAsp 333
Db      362 TACCTGTCCAAAGCGGGGCGCTGCTGGCAGGACCTTGGAGTCCACATCATATGAC 421
Qy      334 LeuLeuPheThrValPheSerLysGlyGluLysArgLysMetLysSerLeuAspGluSer 353
Db      422 CTGCTCTTACCGCTTCTTCCAAAGGCGCAAGCGGAAATCAATCCCTGATAGTCG 481
Qy      354 AlaLeuCysIlePheIleLeuLysGluIleAsnAspArgIleLysGluArgLeuGlnSer 373
Db      482 GCCCTGTGATCTTCACTTGAAGCAGATTAATGACCCCATTAAGACCGGCTGCAGTCT 541
Qy      374 CysTYrARgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys 393
Db      542 TGTACCGGGGCGACGGGCGACGCTGACCTGGCTGGCTGAAGGATCAATCCCTCCG 601
Qy      394 SerSerAlaLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetSerAlaProLeu 413
Db      602 AGCAGTGGCTCTTAAACCATTAACGATACCTTGCTGGCTGACATGAATGCTCCCTG 661
Qy      414 GluValSerAspMetValARgGlyIleProValPheThrGluAspArgAspArgMetThr 433
Db      662 GGAATGTCACATGATGAGCTGATTCCTGCTTCAAGGAGACAGGAGCGGATGAG 721
Qy      434 SerValIleAlaIleValIleValAsnHisSerLeuAlaPheValGlyThrLysSerGly 453
Db      722 TCTGTATCCCATATGTCTCAAGAACCACTCTGCTTGTGGGCAACAAAGTGGC 781
Qy      454 LysLeuLysLysIle 458
Db      782 AACCTGAAGAGGTG 796

RESULT 10
US-10-245-771-91
; Sequence 91, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
US-10-245-771-91

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/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 91
/ LENGTH: 2597
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-245-851-91
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Alignment Scores:
Pred. No.: 1.06e-137 Length: 2597
Score: 1372.00 Matches: 264
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.62% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: Gaps: 14
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US-09-964-956-13 (1-1896) x US-10-245-851-91 (1-2597)

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QY 194 GluTrpRheProThrIleSerSerArgLysLeuThrIleYsaNsSerGluAlaAspGlyMet 213
DB 2 GAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAGT 61
QY 214 PheAlaIYrValPheHIsaSpGluPheValAlaSerMetIleYsaIleProSerAspThr 233
DB 62 TTCGCGTACGCTTCCAGATGAGTTGTTGCTTCGATGATTAGATTCCTTGGACACC 121
QY 234 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPro 253
DB 122 TTCACCATCATCCCTGATCTTGAATCTACTAATGCTATGTTTGGAGTGGCACTTT 181
QY 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrIleYsa 273
DB 182 GTTACTCTTTTGACCCCTCCACCATGAGATGTTCTTCCACAGCTCCACCAAGAGAG 241
QY 274 GluAlaTyrThrSerIleYsaIleValArgLeuGlyLeuAspThrAlaPheAsnSerTyr 293
DB 242 CAGGTGATATCATCTCAAGCTCGTGAAGCTTTGCAAGAGAGACACAGCTTCACTCTAT 301
QY 294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuGlnAlaAla 313
DB 302 GTAGAGGTGGCCATTTGCTGTGAGCGAGTGGGTGAGTACCGCTCGAGGCTGCC 361
QY 314 TyrLeuSerIleYsaIleValAlaValLeuGlyArgThrLeuGlyValHisProAspAsp 333
DB 362 TACCTGTCCAAAGCGGAGCGGCGTCTTGGCAAGACCTTGAATCCATCCAGATGATGAC 421
QY 334 LeuLeuPheThrValPheSerIleYsaIleGlnLysArgLysMetIleYsaIleAspGlu 353
DB 422 CTGCTCTTCAACCGCTCTTCCAAAGGCGCAGAGGCGAAATGAAATCCCTGATGATGCG 481
QY 354 AlaLeuCysIlePheIleLeuLysGlnLysAsnAspArgLysGluArgLeuGlnSer 373
DB 482 GCCCTGTGATCTTCAATCTTGAAGCAATTAATGACCGCTTAAAGACCGGCTGCACTT 541
QY 374 CysTyrArgGlyGlnGlyThrLeuAspLeuAlaTyrPheLysValIleYsaPheIlePro 393
DB 542 TGTATACGGGGGCGAGGCGACGCTGACCTGGCTGCTCAAGGTGAAGGACATCCCTGCG 601
QY 394 SerSerIleLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetAsnAlaProLeu 413
DB 602 AGCGGTGGCTCTTAACCATTAAGACATTAATCTTCTGTGCGCTTGAATGATGCTCCCT 651
QY 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspMetThr 433
DB 662 GGAATGTCCGACATGAGTGGCGTGAATCCGCTTTCACGAGGAGCAGGAGCCCATGACG 721
QY 434 SerValIleAlaIleTyrValTyrLysAsnHisSerIleuAlaPheValGlyThrIleYsa 453
```

```
DB 722 TCTGTCATCGCATATGTCATACAAAGACCATCTCTGGCCTTTGAGGACCAAAAGTGGC 781
QY 454 LysLeuLysLysIle 458
DB 782 AAGCTGAAGAAAGTGG 796
```

RESULT 12  
US-10-245-883-91

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/ Sequence 91, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Batson, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guiney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Pong Sherman
```

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C70

CURRENT FILING DATE: 2002-09-16  
PRIOR FILING DATE: 2002-07-18  
PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116

SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-883-91

Alignment Scores:  
Pred. No.: 1.06e-137 Length: 2597  
Score: 1372.00 Matches: 264  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.62% Mismatches: 0  
Query Match: 13.73% Indels: 0  
DB: Gaps: 14

US-09-964-956-13 (1-1896) x US-10-245-883-91 (1-2597)

```
QY 194 GluTrpRheProThrIleSerSerArgLysLeuThrIleYsaNsSerGluAlaAspGlyMet 213
DB 2 GAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAGT 61
QY 214 PheAlaIYrValPheHIsaSpGluPheValAlaSerMetIleYsaIleProSerAspThr 233
DB 62 TTCGCGTACGCTTCCAGATGAGTTGTTGCTTCGATGATTAGATTCCTTGGACACC 121
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QY 224 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPro 253  
DB 122 TTCACCATCATCTCCGACTTGTATGATCTATGCTATGCTTATGAGTGGCAACTTT 181  
QY 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThrLeuGlu 273  
DB 182 GCTTCTTTTTCACCTTCCACCTGATGATGCTGCTTCCACCGAGCTCCACCAAGGAG 241  
QY 274 GlnValTyrThrSerIleValIleArgLeuCysIleAspThrValPheAsnSerTyr 293  
DB 242 CAGGTGTATACATCCACAGCTCGTAGGCTTTGCAAGAGAGACACAGCTTCACTCAT 301  
QY 294 ValGlnValProIleGlyCysGlnArgSerGlyValGluTyrArgLeuLeuGlnAla 313  
DB 302 GTAGAGGTGCCATTTGGCTGTGAGCGAGTGGGGAGTACCGCTGCTGCAAGGCTGCC 361  
QY 314 TyrLeuSerIleAlaGlyValIleValLeuGlyArgThrLeuGlyValIleProAspAsp 333  
DB 362 TACCTGTCCAAAGCGGGCGCGGTGTGGCAGGACCTTGGAGTCCATCCAGATGATGAC 421  
QY 334 LeuLeuPheThrValPheSerIleGlyGlnIleArgIleMetIleSerLeuAspGlnSer 353  
DB 422 CTGCTCTTCAACCGTCTTCTCCAAAGGCCGAAAGCGGAAATGAAATCCCTGATGAGTGC 481  
QY 354 AlaLeuCysIlePheIleLeuIleAspAspArgIleLeuGlyValArgLeuGlnSer 373  
DB 482 GCCCTGTGATCTTCTTCTGAAAGCATGATGACCGGATTAAGAGAGCGGTGACGCT 541  
QY 374 CysTyrArgGlyGlyGlyThrLeuAspLeuAlaTyrPleuIleValIleAspIleProCys 393  
DB 542 TGTATCCGGGGCGGCGGACGCTGACCTGGCTGCTCAAGATGAAAGCATCCCTGGC 601  
QY 394 SerSerAlaLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetAsnIleProLeu 413  
DB 602 AGCAGTGGCTCTTACCATTTGACATGATGATCTTGTGGCTGACATGATCTCCCTG 661  
QY 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr 433  
DB 662 GAGGTGCCGACATGTGGTGGTGAATTCCTGCTTACGAGAGACGAGGACGCACTGACG 721  
QY 434 SerValIleAlaIleThrValTyrIleAsnIleSerLeuAlaPheValGlyThrIleSerGly 453  
DB 722 TCTGTATCGCATATGCTCAAGAACACTCTCTGCTTGTGGGACCAAAAGTGGC 781  
QY 454 IysLeuIleIleIle 458  
DB 782 AAGCTGAGAAAGCTG 796  
RESULT 13  
US-10-237-535-91  
Sequence 91, Application US/10237535  
Publication No. US20030073188A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Matabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Feng, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C3  
CURRENT APPLICATION NUMBER: US/10/237,535  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091358  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/123957  
PRIOR FILING DATE: 1999-03-12  
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PRIOR FILING DATE: 1999-03-11  
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PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/131271  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/133459  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/135725  
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PRIOR FILING DATE: 1999-05-25  
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PRIOR FILING DATE: 1999-07-26  
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PRIOR FILING DATE: 1999-08-12  
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PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149395

PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/150114  
PRIOR FILING DATE: 1999-08-20  
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PRIOR FILING DATE: 2000-01-20  
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PRIOR FILING DATE: 2000-02-02  
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PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
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PRIOR FILING DATE: 2000-04-18  
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PRIOR FILING DATE: 2000-04-25  
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PRIOR FILING DATE: 2000-05-23  
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PRIOR FILING DATE: 2000-09-15  
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PRIOR FILING DATE: 2000-09-22  
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PRIOR FILING DATE: 2001-01-12  
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PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
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PRIOR FILING DATE: 2001-03-09  
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PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/282129  
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PRIOR APPLICATION NUMBER: 09/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
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PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
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PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09

Alignment Scores:  
Pred. No.: 1,06e-137 Length: 2597  
Score: 1372.00 Matches: 264  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.62% Mismatches: 0  
Query Match: 13.73% Indels: 0  
DB: 14 Gaps: 0

US-09-964-956-13 (1-1896) x US-10-237-535-91 (1-2597)

QY 194 GIUTYRPHETPHTHLETSERARGLYBLUTHRYSAENSERGLUALAASPGLYMET 213  
DB 2 GNGHATTTTCCACCATTCACGCCGGAATGACCAAGACTGTAGGCCGATGCGCATG 61  
QY 214 PHEALATYVALPHEHISASPGIUPHEVALALASERNETILEYSLIEPROSERASPTHR 233  
DB 62 TTCGGGTACGCTTCCATGATGAGTTCGTGCGCTCGATGATTAGATCCCTTCGACACCC 121  
QY 224 PHEHTRIELLEPROASPHEASPILETTYRVALTYRGLYPHESERSEGLYASNPHE 253  
DB 122 TTCACCATTCCTCCGACTTGATTTGATTTACTATGTCTATGTTTGTAGGAGGCACTTT 181  
QY 254 VALTYRPHLEUTHRLEUGINPROGLUWETVALSERPROFGLYSETHRTHLYSGIU 273  
DB 182 GTCACCTTTTGACCTTCAACCTGACGATGCTGCTCACACGAGCTCACCAAGGAG 241  
QY 274 GINVALTYRTHSERLYSLEUVALARGLEUCYELYSGLUASPTTHRALPHASNSERTYR 293  
DB 242 CAGGTGTATACATCCMAAGCTGTGAGGCTTTGCAAGGAGACACGCTTCACTCTCAT 301  
QY 294 VALGIUVALPROILEGLCYEGIUNRSESGLYVALGIUTYRATGLEUGINALAIA 313  
DB 302 GTAGAGGTGCCATTCGTGTGAGGCGAGTGGGGGAGTAGACCGCTGCTCAGGCTGCC 361  
QY 314 TYRLEUSERLYSALAGLYALAVALLEUGLYARGTHRLEUGLYVALHISPRCASPSASP 333  
DB 362 TACCTGTCCAAAGCGGGGCGGTGCTTGCGAGGACCTTGAGTCCATTCAGATGATGAC 421  
QY 334 LEULPHEPTHNVALPHESERLYSGIUNYSAATGLYSMETLYSSETHLEUASPIUBER 353

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Db 422 CTCCTCTTCACCGCTCTTCTCCAGGGCCAGAAACGGAAATGCCCTGATGATGTC 481
Qy 354 AAlaLeuCySlePheIleLeuYsgInIleAsnAspArgIleGlyGluuArgLeuGlnser 373
Db 482 GCCCTGTGATCTTCTTCTTGAAGCAGATATGACCGCATTAAGAGGGCGGTGACAGTCT 541
Qy 374 CyETyArgGlyGluGlyThrIleuAspIleuAlaITPLeuYsValIysAspIleProCys 393
Db 542 TGTTCACGGGGCCAGGGACGCTGACCTGGCTGCTCAGGTGAGGACATCCCTGTC 601
Qy 394 SerSerAlaLeuLeuThrIleAspAspAspPheCysGlyLeuAspMetSerAlaProLeu 413
Db 602 AGCAGTGGCGCTTTAACCATTCGATTCGATTCCTGCGCTGACATGAAATCTCCCTGC 661
Qy 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspMetThr 433
Db 662 GAGTGTCCGACATGGCGGTGGATTCCTGCTTCCAGGAGGACAGGACCGCATGACG 721
Qy 434 SerValIleAlaTyrtValTyrtIysAsnHisSerLeuAlaPheValGlyThrIysSerGly 453
Db 722 TCTGTATCCGATATGCTTACAAAGACCACTCTGCGCTTGTGGCACCAAAAGTGGC 781
Qy 454 IysLeuYsIle 458
Db 782 AAGCTGAGAAAGGTG 796

RESULT 14
US-10-238-183-91
/ Sequence 91, Application US/10238183
/ Publication No. US20030073189A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Metabee, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zhenli
/ APPLICANT: Feng, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C11
/ CURRENT APPLICATION NUMBER: US/10/238,183
/ CURRENT FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: 10/187942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
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/ PRIOR APPLICATION NUMBER: 60/065027
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/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
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/ PRIOR APPLICATION NUMBER: 60/170262
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/ PRIOR APPLICATION NUMBER: 60/171118
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/ PRIOR APPLICATION NUMBER: 60/180921
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PRIOR FILING DATE: 2001-01-16  
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PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/266421  
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PRIOR FILING DATE: 2001-03-09  
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PRIOR APPLICATION NUMBER: 60/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/872035  
PRIOR FILING DATE: 2001-06-01  
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PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 60/946374

PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09

Alignment Scores:

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Score:	1372.00	264
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Best Local Similarity:	99.62%	0
Query Match:	13.73%	0
DB:	14	0

US-09-964-956-13 (1-1896) x US-10-238-183-91 (1-2597)

QY 194 GlnTyrPheProThrIleSerSerArgLysLeuThrIleAsnSerGlnAlaAspGlyMet 213

Db 2 GAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGACTCTGAGCGGATGGCATG 61

QY 214 PheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr 233

Db 62 TTCCGCTACGCTCTTCATGATGATGCTGAGCGCTCGATGATTAAGATCCCTTCGACACC 121

QY 234 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPhe 253

Db 122 TTCACCATCATCCCTGACTTGATGATCTATGATGATGATGATGATGATGATGATGATGAT 181

QY 254 ValTyrPheLeuThrIleGluPheProGluMetValSerProProGlySerThrThrLysGlu 273

Db 182 GTTACTTTTGGACCTCCCAACCTGAGATGCTGCTCCACAGGCTCCACCAAGAGAG 241

QY 274 GlnValTyrThrSerLysLeuValArgLysGluAspThrAlaPheAsnSerTyr 293

Db 242 CAGGTATATCATCAAGCTGCTGAGGCTTTCAGAGAGAGACAGGCTTCACTCAT 301

QY 294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLysLeuGlnAla 313

Db 302 GTAGAGTGCCCATTTGGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361

QY 314 TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAsp 333

Db 362 TACCTGTCACAAAGCGGGCGCTGCTGGCAGGACCTTGAGCTCAATCCAGATGATGAC 421

QY 334 LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLysAspGlySer 353

Db 422 CTGCTTCACCGCTTCTTCCAGGGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481

QY 354 AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgLysGluArgLysSer 373

Db 482 GCCCTGTCATCTTCATTTGACAGATTAATGACCGCATTAAGAGCGGCTCAGACT 541

QY 374 CysTyrArgGlyGlyGlyThrLeuAspLeuAlaThrLeuLysValLysAspIleProCys 393

Db 542 TGTATCCGGGCGAGGAGCGCTGAGCTGCTGCTCAAGGAGGAGGAGGAGGAGGAGGAGG 601

QY 394 SerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeu 413

Db 602 AGCATGCGCTCTTAACCATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 661

QY 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspAspAspMetThr 433

Db 662 GGAGTGTCGACATGAGTGGGAGTATCCCTTCACGAGGAGGAGGAGGAGGAGGAGGAGG 721

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Db 722 TGTGTCATCGCATATGTTTACAAAGACCACTCTGGGCTTGGGAGGAGGAGGAGGAGG 781

QY 454 LysLeuLysLysIle 458



DB 782 AACCTGAAGAAAGTGTG 796

RESULT 15  
US-10-238-283-91

Sequence 91, Application US/10238283  
Publication No. US20030073190A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Bacon, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Watande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C15

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

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PRIOR FILING DATE: 1998-03-27

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QY 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThrIleValGlu 273

DB 182 GTCTACTTTTGGACCCCTCCACCTGAGATGTGTCTCCACAGGCTCCACACCAAGAG 241

QY 274 GluValTyrThrSerIleValValArgLeuCysIleValGlnAspThrAlaPheAsnSerTyr 293

DB 242 CAGGTGTATCATCTCAACCTCGTGAAGCTTTGCAAGAGGACACAGCTTCACTCTAT 301

QY 294 ValGluValProIleGlyCysGluArgSerGlyValGlnTyrArgIleLeuGlnAla 313

DB 302 GTAGAGGTGGCCATTTGGCTGTGAGCGGAGTGGAGTACCGCTGTCAGAGCTGCC 361

QY 314 TyrLeuSerIleValIleValAlaValLeuGlnValArgThrIleGlnValHisProAspAsp 333

DB 362 TACCTGTCCAAAGCGGCGGCGTGTGGAGACCTTGAGAGCTTCATCCATGATGAC 421

QY 334 LeuLeuPheThrValPheSerIleGlyGlnIleAsnAspArgIleValGluArgLeuGlnSer 353

DB 422 CTGCTCTTCAACCGCTTCTCCAAAGGCGGAGAAATGAAATCCCTGATGATGTCG 481

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DB 482 GCCCTGTGATCTTCACTTGAAGCAGATTAATGACCGCATTAAGAGCGGCTGCACTCT 541

QY 374 CysTyrArgIleGlyGlnIleValLeuAspLeuAlaTrpLeuValIleAspIleProCys 393

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DB 602 AGCAGTGGCTCTTAACCATTTGACGATTAACCTTGTGGCTGACATGAATGCTCCCTG 661

QY 414 GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr 433

DB 662 GAGTGTCCGACATGAGTGGCTGGAATCCGCTTTCACGAGGACAGGACCCCATGACG 721

QY 434 SerValIleAlaIleTyrValIleValAsnHisSerLeuAlaPheValGlyThrIleValSerGly 453

DB 722 TCTGTGATCGATATGTCTCAAGAACCACTTCTGTGGCTTGTGGGACACCAAAAGTGGC 781

QY 454 LysLeuIleValIle 458

DB 782 AACCTGAAGAAAGTGTG 796

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US-09-964-956-13 (1-1896) x US-10-238-283-91 (1-2597)

QY 194 GluTyrPheProThrIleSerSerArgIleuThrIleAsnSerGluAlaAspGlyMet 213

DB 2 GATGATTTTCCACCATCTCCACCGGAACGACCAAGAACTGTAGCGGATGGCATG 61

QY 214 PheAlaIleTyrValPheHisAspGluPheValAlaSerMetIleValIleProSerAspThr 233

DB 62 TTGGCGTACGCTCTTCATGATGATCGTGGCTCGATGATTAAGATCCCTTCGACACG 121

QY 234 PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPhe 253